Adb54249 Pretreate
Ab133421 Human imm
Aa180765 Human pol
Ab48845 Oligonucl
Ab48444 Oligonucl
Ab40450 Colon pro
Ab133823 Human imm
Ab133724 Human imm

Scoring table:

Searched:

Seguence:

Minimum DB Maximum DB

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Run on:

Abg13708 Oligonucl Abg13709 Oligonucl Abn80108 Human che Ab170466 Chemicall Aas61457 Human gen

.av64065 Zea mays Adx60794 Plant ful Adm47619 Polynucle

Abx87875 Corn ear

Add54826 Novel can Ada19123 Rice DNA Ada47694 Bacterial Ada46575 Tumour su Ab133832 Human imm Ab133555 Human imm Ab133555 Human mer

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This sequence represents a 3' untranslated region (UTR) which was used in the construction of the recombinant expression cassette of the invention. The expression cassette is for effecting expression of a foreign gene in a transformed plant and comprises a promoter operable in plants, an untranslated leader sequence, a foreign gene of interest, and a 3'UTR. This cassette may be used to transform plants, for genetic engineering of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated DNA molecule useful for genetic engineering of plants or for improving the expression of transgenes in plants, particularly corn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; 3' untranslated region; UTR; expression cassette; transformed plant; promoter; untranslated leader sequence; genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                      ABQ13708
ABQ13709
ABN80108
ABL70466
AASG1457
ADB54249
ABL33421
ABL33421
ABC48845
ABQ48845
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ABQA884
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ADS47694
AAS46575
ABL33832
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ABL34571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI22022 standard; DNA; 332 BP
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Adx30934 Plant ful
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                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                      nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                  recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactoromannan production; lignin production; plant growth regulator; yield; plant growth, plant development; seed oil; protein yield; protein content; gene; se.
                                                                                 1 GGTCGCAGCGTGTGCGTGTCCGTAACGTTCTGGCCGGCCCGGGCCTTGGGCCGCGCGATC
                                                                                                     CAAGGTGGATCGCGTGTCAAGGCCCGTGTGTTTAAANACCCACCGGCACTGGCAGTGA
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plants or in improving the expression of transgenes in plants
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                 Sequence 332 BP; 51 A; 62 C; 100 G; 116 T; 0 U; 3 Other;
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                                 100.0%; Score 329; DB 12;
100.0%; Pred. No. 7e-91;
ive 0; Mismatches 0;
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05-NOV-2001; 2001US-00985678.
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                                          al Similarity 100.
332; Conservative
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one state of the content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert properties of the plant of the recombination to the cost of the content. This sequence represents a plant full length insert properties.
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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
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Pred. No. 1.2e-90;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1236 BP; 288 A; 333 C; 405 G; 210 T; 0 U; 0 Other;
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                                                                                                                                                                                     Claim 1; SEQ ID NO 13754; 15pp; English.
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                                                                                                            improving yield.
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61 AGAANCGTTGCGTTGGCGTGTGTGTGTG

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the production of immunoglobulins in plants, wherein at least a portion of the glycans attached to the immunoglobulins to lack fucose. The immunoglobulins produced can be of any class (i.e., IgG, IgA, IgM, IgB or IgD) and is especially an anti-herpes simplex virus (HSV) antibody or an anti-alphaVbeta3, alphaVbeta5 dual integrin antibody. The invention also relates to constructs, plasmids and vectors corp producing the immunoglobulins; transformed plant cells, calli, plant tissues and whole plants for producing the immunoglobulins, the immunoglobulins; methods for producing the immunoglobulins of the invention use of such immunoglobulins. The immunoglobulins of the invention may be used to treat HSV infection or tumour angiogenesis. The invention production, the invention of provides the advantages of antibody production in plants, such as large contaminants such as viruses and elimination of pathogenic contaminants such as viruses and elimination of pathogenic contaminants such as viruses and prions, with a simplified (i.e., non-plant specific) glycosylation profile which reduces the risk that the immunoglobulin may not be functional in animals. The present sequence represents the plasmid pubasol4, which may be used in the invention. The plasmid contaminants and contaminants for a plant specific players and contaminants for a plasmid pubasol4, which may be used in the invention. The plasmid contaminants and contaminants and contaminants and contaminants and contaminants and contaminants in the invention. The plasmid contaminants and con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel plant-produced immunoglobulin having glycopeptide or glycan profile with reduced fucosylation, useful for treating herpes simplex virus
                                                                                                                                                                                                                                                                                                                            /*tag= c
/note= "Maize lipase 3'UTR. The 3' end of this 3'UTR has
been deduced from that given for pDAB8505 (SEQ ID NO:85),
as the 3'UTR location given for this plasmid is 2296-
652."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glancy T, Hein MB, Hiatt AC, Karnoup AL, Anderson WHK; Petolino J, Rubin-Wilson B, Taylor D, Roberts JL;
                                                                                                                                                                                                                                                    /*tag= b
/product= "Phosphinothricin acyltransferase (PAT)"
2296. .2627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5118 BP; 1240 A; 1256 C; 1286 G; 1336 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 329; DB 12; Length 5118; Pred. No. 2.1e-90; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                control of a rice actin promoter, and a maize lipase 3'UTR
                                                                                                                                                                                                         "Rice actin promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 69; SEQ ID NO 84; 212pp; English.
                                                                                                                                      Location/Qualifiers
1172. .1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.1%;
Matches 329; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
(EPIC-) EPICYTE PHARM INC.
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                                                                                                                                                                                                           'note=
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                       Oryza sativa,
                                                                   Synthetic.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-2004
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Pareddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection.
  Zea mays.
                                             Chimeric
                                                                                                                                                              promoter
                                                                                                                                                                                                                                                                                                  3' UTR
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δ g

Gaps

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2476 GTGTTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT 2535
                                                                                                                                  2536 ACTACTTGGGTTTGTTGATTATTGAGCAGTTGCGTATTGTAATTCAGCTGGGCTACC 2595
                                                                      240
                                                                                                              241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
                                           2416 CAAGGIGGATCGCGIGGICAAAGGCCCGIGTGCTITAAAGACCCACCGGCACTGGCACTGGCAGTGA
                                                                                                                                                                                                                                                                                                                  GnTIII; N-acetylglucosaminyltransferase; transgenic; glycoprotein; ds.
                                                                       GTGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGCTTTATTTGCTTCTGGATGTTGTGT
                             CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGTGAANACCCACCGGCACTGGCAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= c
note= "rice actin promoter and intron"
235. .2696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= 1
/note= "linker sequence (ACF58355)"
5130. .7523
                                                                                                                                                                                                                                                                                                                                                                                                                *tag= b
note= "linker sequence (ACF58351)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "linker sequence (ACF58353)"
                                                                                                                                                                         2596 TGGACATTGTTATGTATTAATAAATGCTTTGC 2627
                                                                                                                                                        TGGACATTGTTATGTATAATAATGCTTTGC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rag= d
note= "rice actin intron"
704. .3258
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .1146
/*tag= a
/note= "tobacco Rb7 MARs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= g
note= "maize lipase UTR"
omplement(3671. .4836)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= i
note= "tobacco Rb7 MAR"
                                                                                                                                                                                                                                                                                             Nucleotide sequence of plasmid pDAB8504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Puc19"
104. .5130
                                                                                                                                                                                                                                 ACF58343 standard; DNA; 7545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .4857
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*tag= h
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                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                             121
                                                                      181
                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3'UTR
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GnIIII; N-acetylglucogaminyltransferase; transgenic; glycoprotein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note = "ampicillin resistance gene"
                                            Nucleotide sequence of plasmid pDAB7113.
                                                                                                                                                                                                                       /.rag= d
/note= "GNTIII v.2"
4896. .5260
                                                                                                           Location/Qualifiers
1. .1164
/*tag= a
/note= "Rb7 MAR v3"
                                                                                                                                                                                                                                                                                                                                                 6803. .7358
/*tag= h
/note= "PAT v3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Puc19"
10164. .11021
/*tag= n
                        12-FEB-2004 (first entry)
                                                                                                                                                                                                *tag=
'note= "
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                                                                                                                    misc_feature
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                                                                                       Synthetic
  ACF58344;
                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                  3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                3'UTR
   THE STANKE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3513 ACTACTIGGGTITGTIGAATTATTATGAGCAGTIGGGGTATTGTAATTCAGCTGGGCTACC 3572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                           New plant host cell system for producing a desired glycoprotein comprises a mammalian N-acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic acid sequence encoding the enzyme, or a vector comprising the nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
                                                                                                                                                                                                                                                                                                   The invention relates to a plant host cell system comprising a mammalian UDP-N-acetylglucosamine: beta-D mannoside beta(1,4)-N-acetylglucosamine: beta-D mannoside beta(1,4)-N-acetylglucosaminyltransferase (GATIII) enzyme, a nucleic acid sequence encoding a mammalian GATIII protein, or a vector comprising the GATIII nucleic acid. The plant host system is useful in producing a desired glycoprotein or its functional fragment. The glycoprotein or its functional fragment may be used for the production of a pharmaceutical composition. The present sequence represents the nucleotide sequence of plasmid pDABBS04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3393 CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGTTTAAAGACCCACCGGCACTGGCAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGGTGGATCGCGTGAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTTATTTGCTTCTGGATGTTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7545 BP; 2128 A; 1579 C; 1622 G; 2216 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                /*tag= n
/note= "linker sequence (ACF58356)"
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 329; DB 10;
Pred. No. 2.4e-90;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3573 TGGACATTGTTATGTATTAATAAATGCTTTGC 3604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGACATTGTTATGTATTAATAATGCTTTGC 332
                                                                                                                                                                                     Bosch HJ;
                                                                                                                                                                                                                                                                                 Example 6; Fig 7B; 122pp; English.
/*tag= m
/note= "Puc19"
7524. .7545
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
99.1%; P
                                                                                                                              19-MAR-2002; 2002US-0365769P.
26-MAR-2002; 2002US-0368047P.
                                                                                                          18-MAR-2003; 2003WO-IB001562
                                                                                                                                                                                   Florack DEA,
                                                                                                                                                             (PLAN-) PLANT RES INT BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.1
Matches 329; Conservative
                                                                                                                                                                                                        WPI; 2003-779132/73.
                                                                WO2003078614-A2
                       misc feature
                                                                                      25-SEP-2003
                                                                                                                                                                                  Bakker HAC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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note= "multiple cloning sites (ACF58358)" 405. .6802

*tag=

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*tag= g note= "rice actin 1 promoter

.7358

*tag= e note= "maize peroxidase-5 3'-UTR" 261. .5404

*tag= i note= "linker sequence (ACF58359)"

.7372

UTR"

*tag= j note= "maize lipase

.7729

.7770

*tag= note= *tag=

(ACF58360)"

"linker sequence

٧3 ٿ

note= "Rb7 MAR 935. .11643

*tag= b note= "linker sequence (ACF58357)" 234. .3224

.1233

promoter"

c "maize ubiquitin 1

.4891

225. .4 *tag=

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New plant host cell system for producing a desired glycoprotein comprises a mammalian N-acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic acid sequence encoding the enzyme, or a vector comprising the nucleic acid sequence.
                                                                                                                                                                                                                                              Bosch HJ;
                                                             19-MAR-2002; 2002US-0365769P.
26-MAR-2002; 2002US-0368047P.
18-MAR-2003; 2003WO-IB001562
                                                                                                                                                                                                                                          Bakker HAC, Florack DEA,
                                                                                                                                                                      (PLAN-) PLANT RES INT BV.
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ACF58344 ID ACF58344 standard; DNA; 11643 BP XX

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Novel plant-produced immunoglobulin having glycopeptide or glycan profile with reduced fucosylation, useful for treating herpes simplex virus infection.
                                                                                                                                             monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                 chain of human anti-HSV1/HSV2 monoclonal (with mouse leader sequence)"
             /note= "Scaffold attachment region. Also referred to as MAR (matrix association region)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Scaffold attachment region. Also referred to as MAR (matrix association region)"
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Taylor D, Roberts JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PAT)"
                                                                                                                                         chain of human anti-HSV1/HSV2 (with mouse leader sequence)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product= "Phosphinothricin acyltransferase ()
note= "The PAT coding region is given in the
pecification as positions 9260-9820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Rice actin promoter/intron"
                                                                      *tag= b
note= "Maize gamma-zein promoter"
                                                                                                                                                                                                                                                                                                                                                                *tag= g'
note= "Maize gamma-zein promoter"
                                                                                                                                                                                                                                                                   "Mature HX8 heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mature HX8 heavy chain"
                                                                                                                                                                                                              "Mouse leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Mouse leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Maize lipase 3'UTR"
0229. .11394
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J, Rubin-Wilson B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Maize per5 3'UTR"
                                                                                                                                                                                                                                                                                                                       "Maize per5 3'UTR
                                                                                                                                        product= "Heavy
gA antibody HX8
                                                                                                                                                                                                                                                                                                                                                                                                                               product= "Heavy
gA antibody HX8
                                                                                           /*tag= /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
(EPIC-) EPICYTE PHARM INC.
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label= SAR
label= SAR
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P-PSDB; ADP73848, ADP73856.
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note= '
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Petolino
                                                                                                                                                                           78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 29
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                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                           mat_peptide
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Pareddy D,
                                                      promoter
                                                                                                                                                                                                                                                                                                                                           promoter
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                                                                                                      CDS
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                                                                                                                                                                                                                                                                                                                                                                           7373 GGTCGCAGCGTGTGCGTGTCCGTCGTTCTGGCCGGCCGGGCCTTGGGCGCGCGATC 7432
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                                                                                                                                                                                                                                                                                                                                                                                                                                   7672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
                                                                                                                                                                                                                                                                                                                                         9
                                                  system comprising a mammalian
                                          The invention relates to a plant host cell system comprising a mammaliar UDP-N-acetylglucosamine: beta-D mannoside beta(1,4)-N-acetylglucosamine: beta-D mannoside beta(1,4)-N-acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic acid sequence encoding a mammalian GnTIII protein, or a vector comprising the GnTIII nucleic acid. The plant host system is useful in producing a desired glycoprotein or its functional fragment. The glycoprotein or its functional fragment may be used for the production of a pharmaceutical composition. The present sequence represents the nucleotide sequence of plasmid pDAB7113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic plant; immunoglobulin production; recombinant production; glycosylation; fucose; glycan; virucide; immunotherapy; maize; gamma-zein promoter; rice; actin promoter; phosphinothricin acyltransferase; PAT; mouse; leader sequence; herpes simplex virus; HSV1; HSV2; human; monoclonal antibody HX8; IgA; heavy chain; light chain; codon optimised; plasmid; pDABBSO5; cyclic; circular; ds.
                                                                                                                                                                                                                                                                                                                                        7553 GIGTIGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGTTTAAANACCCACCGGCACTGGCAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGTTGCTGCTTGTGAGGCTTTGGTACGTATGGCTTTTATTTGCTTCTGGATGTTGTGT
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                             Sequence 11643 BP; 3005 A; 2672 C; 2635 G; 3331 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                   Length 11643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pDAB8505, SEQ ID NO:85, encoding mAb HX8 (both chains)
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                    Score 329; DB 10;
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                                                                                                                                                                                                                                                                                Pred. No. 2.9e
0; Mismatches
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424. .1589
/*tag= a
             6; Fig 8B; 122pp; English
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                                                                                                                                                                                                                                                                 100.0%;
99.1%; E
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                                                                                                                                                                                                                                                                                  Best Local Similarity 99.1
Matches 329; Conservative
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Mus sp.
Homo sapiens.
Oryza sativa.
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Unidentified.
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                                                                                                                                                                                                                                                                   Query Match
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              Example
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ADP73931

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The invention relates to the production of immunoglobulins in plants, wherein at least a portion of the glycans attached to the immunoglobulins completed to the immunoglobulins produced can be of any class (i.e., 1gG, 1gA, 1gM, 1gE or 1gD) and is especially an anti-herpes simplex virus (HSV) antibody or an anti-alphavbeta3, alphavbeta5 dual integrin antibody. The invention also relates to constructs, plasmids and vectors (CC antibody. The invention also relates to constructs, plasmids and vectors for producing the immunoglobulins; transformed plant cells, calli, plant tissues and whole plants for producing the immunoglobulins; the immunoglobulins; methods for producing the immunoglobulins, the immunoglobulins of the invention cuse of such immunoglobulins or tunour anglogenesis. The invention may be used to treat HSV infection or tunour anglogenesis. The invention contaminants such as viruses and pricons, with a simplified (i.e., non-plant-specific) glycosylation profile which reduces the risk that the plant average of encional in animals. The present sequence represents the plasmid phabas50s, which contains codon optimised DNA sequences encoding the heavy and light chains of the human anti-HSV1/HSV2 of manice endosperm-specific gamma-zein promoters. The plasmid also contains a phosphinotricin acyltransferase (PAT) gene under the control of a rice and promoters. The plasmid also
                          Claim 69; SEQ ID NO 85; 212pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a rice actin promoter.
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ö 120 9 0; Gaps Sequence 13680 BP; 3886 A; 3069 C; 2934 G; 3788 T; 0 U; 3 Other; Length 13680; Indels ; Score 329; DB 12; ; Pred. No. 3.1e-90; 0; Mismatches 0; 100.0%; Query Match
Best Local Similarity 100.
Matches 332; Conservative ò 셤 ò

10070 10071 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 10130 10010 9950 180 240 300 CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTTAAANACCCACCGGCACTGGCAGTGA GTGTTGCTGCTTGTGTAAGGCTTTGGTAAGGGCTTTAATTTGCTTCTGGATGTTGTGT CAAGGTGGATCGCGTGGTCAAGGCCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA GTGTTGCTGCTTGTGTAGGCTTTTGGTACGTATGGGCTTTTATTTTGCTTCTGGATGTTGTGT ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 9951 121 181 1001 241 Б ò g ð g ð 원 ò

ADX61274 standard; cDNA; 1206 RESULT 7 ADX61274

(first entry) 21-APR-2005

Plant full length insert polynucleotide segid 32117.

plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat trolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance;

New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; Cao Tabaska JE, Screen SE, 06-MAY-1999; 99US-00304517. 05-NOV-2001; 2001US-00985678. 28-APR-2003; 2003US-00425114. Kovalic DK, protein content; gene; ss WPI; 2004-180133/17. LIU J.
ZHOU Y.
KOVALIC D K.
SCREEN S E. TABASKA J improving yield. US2004034888-A1. Zhou Y, CAO Y. Unidentified 19-FEB-2004. (TABA/) (CAOY/) (KOVA/) (SCRE/) (/rnra) Liu J,

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the sequence. The sequence is useful for a plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease. For producing galactomannan. Iignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the Claim 1; SEQ ID NO 32117; 15pp; English.

Sequence 1206 BP; 281 A; 337 C; 395 G; 193 T; 0 U; 0 Other;

invention

Query Match

DB 13; Length 1206;

Gaps ö 4; Indels Score 327.4; DB 1. Pred. No. 3.6e-90; 0; Mismatches 4 ,0 99.5%; Conservative Best Local Similarity Matches 328; Conserv

926 120 9

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Indels

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180

240

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ADX10934;

ADX10934 RESULT

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1172 ACTACTTGGGTTTGTTGAATTATTATGAGCAGTTGCGTATTGTAATTCAGCTGGGGCTACC 1231
content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
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                                                                                                                                                                                                                                                                                                                                      CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT
                                                                                                                         DB 13; Length 1271;
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                                                                              Sequence 1271 BP; 295 A; 350 C; 412 G; 214 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant full length insert polynucleotide seqid 5169.
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                                                                                                                       Score 327.4; I
Pred. No. 3.7e-
0; Mismatches
                                                                                                                         99.5%;
98.8%;
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05-NOV-2001; 2001US-00985678
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                                                                                                                                           Best Local Similarity 98.8
Matches 328; Conservative
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SCREEN S E.
TABASKA J E.
CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou Y,
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ZHOU Y.
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                                           invention.
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                                                                                                                         Query Match
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(ZHOU/)
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(SCRE/)
(TABA/)
(CAOY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in meletronic form from the US patent office at available in electronic form from the US patent office at the sequence uspto. 2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as the invention are also useful in physical arrays of molecules and as the invention are also useful in physical arrays of molecules and as more in the conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomanan, ignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake condition or for modifying seed oil or protein yield and/or
                                       ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct, useful for improving plant tolerance to cold, hear, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                              plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene;
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                                                                                                 TGGACATTGTTATTAATAAATGCTTTGC 332
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                                                                                                                                                                                                                                               ADX10934 standard; cDNA; 1271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-1999; 99US-00304517
05-NOV-2001; 2001US-00985678
                                                                                                                                                                                                                                                                                                                                 (first entry)
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(ZHOU/) (KOVA/) (SCRE/) (TABA/) (CAOY/)

Liu J,

LIUJ/)

us-10-603-524a-1.rng

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, heatbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert content.
                                                                            New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                  Claim 1; SEQ ID NO 5169; 15pp; English.
                            WPI; 2004-180133/17.
                                                                                                                                                                  improving yield.
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120
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                                                                                  GGTCGCAGCGTGTGCGTGTCCGTACGTTCTGGCCGGCCCGGGCCTTGGGCGCGCGATC
                                                                                                              GGTCGCAGCGTGTGCGTCGTCGTACGTTCTGGCCCGGCCCCTTGGGCGCGCGATC
                                                                                                                                         CAAGGTGGATCGCGTGGTCAAGGCCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA
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                                                         Gaps
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0
                            DB 13; Length 725;
Sequence 725 BP; 149 A; 205 C; 226 G; 145 T; 0 U; 0 Other;
                                                      Indels
                         Score 316.4; DB 1.2 Pred. No. 7.2e-87;
                                                        0; Mismatches
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                          Query Match 96.2%;
Best Local Similarity 98.8%;
Matches 317; Conservative
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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance;
                                                                                                          Plant full length insert polynucleotide seqid 5111.
                           ВЪ.
                         ADX10536 standard; cDNA; 526
                                                                              (first entry)
                                                                              21-APR-2005
                                                     ADX10536;
RESULT 10
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extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell qycle pathway; disease resistence; galactomannan production; lignin disease resistence; galactomannan production; plant growth regulator; grield; plant growth; plant development; seed oil; protein yield;
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                                                                                                                                                                           Cao
                                                                                                                                                                           Tabaska JE,
                                                                                                                                                                           Screen SE,
                                                                                      28-APR-2003; 2003US-00425114.
                                                                                                   06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                                                                                                                          Kovalic DK,
                              protein content; gene; ss
                                                                                                                        LIU J.
ZHOU Y.
KOVALIC D K.
SCREEN S E.
                                                                                                                                                                                       WPI; 2004-180133/17.
                                                                                                                                                     TABASKA J E.
                                                                                                                                                                          Zhou Y,
                                                        US2004034888-A1
                                                                                                                                                             CAO Y.
                                           Unidentified.
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recombinant DNA construct, useful for improving plant tolerance to 1, heat, drought, herbicides, extreme osmotic conditions, pathogens or s, for conferring increased resistance to plant disease, or for improving yield. pests,

Claim 1; SEQ ID NO 5111; 15pp; English.

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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent of fice at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or perse, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, ceombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stream of the content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert of the content. This sequence represents a plant full length insert of the invention

268 120 328 180 181 GTGTTGCTTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTTATTTGCTTCTGGATGTTGTGT 240 9 209 GGTCGCAGCGTGTGCGTGTCCGTACGTTCTGGCCGGCCCGGGCCTTGGGCGCGCGATC CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAAGACCCACCGGCACTGGCAGTGA CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA Gaps ö Score 315; DB 13; Length 526; Pred. No. 1.7e-86; 0; Mismatches 3; Indels C Sequence 526 BP; 95 A; 134 C; 169 G; 128 T; 0 U; 0 Other; 95.7**%**; 99.1**%**; Sest Local Similarity 99.1 Matches 315; Conservative н 329 121 Query Match 셤 ઠે a ઠે 셤

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The invention relates a recombinant DNA construct comprising a polypucide polynucleotide having any of 5544 mucleotide sequences (CDNAs SEQ ID NO: 1-5544) and encoding a polypetide with any of 5544 maino acid sequences (SEQ ID NO: 5455-11088). The CDNAs and proteins are from corn, soybean, a rabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a producing a plant having an improved property, comprising transforming a conductional in a plant cell operably joined to a polymorter region control plant. The property is selected from improving plant cold tolerance, for pathway, for improving plant drought tolerance, for pathway, for improving plant drought tolerance, for pathway, for improving plant drought tolerance. For production of pathway, for improving plant drought tolerance, for production for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for ingroving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for ingroving plant tolerance to extreme osmotic conditions, for improving plant tolerance to bethicides, for increasing the rate of homologous recombination in plants, for ingroving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or peats, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifitying eed protein yield and/or content, for modifitying eed protein yield and/or content, for yield improvement by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osencic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield;
                                                                                                                                                                         449 ACTACTTGGGTTTGTTGAATTATTATGAGCAGTTGCGTATTGTAATTCAGCTGGGCTACC
241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88; gene; transgenic; cold tolerance;
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                                                                                                                                                                                                                                                                                                                                  301 TGGACATTGTTATGTATT 318
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28-APR-2003; 2003US-00425115.
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modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of blochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improved nitrogen flow, increasing plant tolerance to cold or heat, improved nitrogen tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant cDNA sequences of the invention. Note: The sequence data for this patent did not computer form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1191 GTGTACTACTTGGGTTTGTTGAATTATATGAGCAGTTGCGTATTGTAATTCAGCTGGGC 1250
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 301.4; DB 13; Length 1294;
Pred. No. 3.8e-82;
1; Mismatches 5; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1294 BP; 307 A; 351 C; 418 G; 214 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant full length insert polynucleotide segid 1933.
                                                                                                                                                                                                                                                                                                                    electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=20040216190.
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                                                                                                                                                                                                                                                                                                                                                                                                                              91.6%;
97.0%;
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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; se.

28-APR-2003; 2003US-00425114. 06-MAY-1999; 99US-00304517. 05-NOV-2001; 2001US-00985678.

US2004034888-A1.

19-FEB-2004.

Unidentified

S

Plant full length insert polynucleotide seqid 35874.

21-APR-2005 (first entry)

ADX65031;

us-10-603-524a-1.rng

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in meletronic form from the US patent office at available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as the invention are also useful in physical arrays of molecules and as improving plant tolerance to cold, hear, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, ignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosopyntheeds or carbohydrate, nitrogen or phosphorus use and/or uptake conviding improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
                                                                                                                                                                                                                                                                                                            cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of the
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                                                                                                                                                                                                                    Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1057 BP; 242 A; 296 C; 352 G; 167 T; 0 U; 0 Other;
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28-APR-2003; 2003US-00425114,
                                 06-MAY-1999; 99US-00304517, 05-NOV-2001; 2001US-00985678.
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ZHOU Y.
KOVALIC D K.
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Tabaska JE,

Screen SE,

Kovalic DK,

Zhou Y,

Liu J,

CAO Y.

(TABA/) (CAOY/)

WPI; 2004-180133/17.

KOVALIC D K. SCREEN S E. TABASKA J E.

SCRE/) (ZHON/) KOVA/)

LIU J. ZHOU Y.

(FIRT)

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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plantes, for improving yield by modification of photosynthesis or carbohydrate, introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stream of the content. This sequence represents a plant full length insert of the polymore or plant can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTCGCAGCGTGTGCGTCGTCGTACGTTCTGGCCGGGCCG---TTGGGCCGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.9%; Score 286; DB 13; Length 818; 93.4%; Pred. No. 1.7e-77; ive 0; Mismatches 8; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 818 BP; 165 A; 232 C; 257 G; 164 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 35874; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 93.4%;
Matches 324; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
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57

ADX65031 standard; cDNA; 818 BP

RESULT 13

ADX65031

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580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp. seqdata.uspto.gov/sequence.html?bocID:2004034888. The polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                          plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; pest tolerance; galactoomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                  Tricaaggregarcegeregreaggregregregrerraaagacecacegerege
                                                                                                                             ATCAGAAGCGTTGCGTTGGCGTGTGTGTCTCTGGTTTGCTTTAATTTTACCAAGTTTG
                                                      TITCAAGGIGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAG
                                                                                                                                                                     - TCTGGATGTTGTACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAA
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                                                                                                                                                                                                                                              TTCAGCTGGGCTACCTGGACATTGTTATTAATAAATGCTTTGC 807
                                                                                                                                                                                                                              TICAGCIGGCTACCIGGACATIGITATGTATAAAAATGCTTIGC 332
                                                                                                             TGAGTGTTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                  Plant full length insert polynucleotide seqid 5192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 5192; 15pp; English.
                                                                                                                                                                                                                                                                                                                               BB
                                                                                                                                                                                                                                                                                                                              ADX10617 standard; cDNA; 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-1999; 99US-00304517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-2003; 2003US-00425114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2005 (first entry)
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SCREEN S E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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(SCRE/)
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(CAOY/)
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of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 CAAGGTGGGTTCGCGTGGTCAAGGTCCGTGTGCTTTAAAGACCCACCGGCACTGGCAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AGAANCGTTGCGTTGGCGTGTGTGTGTCTGGTTTGCTTTAAFTTTTACCAAGTTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRGTTGCTGCTTGTAGGCTTTGGTACGTATGGGCCTTTATTTGCTTCTGGATGTTGTGT
                                                                                                                                                                                                                                                                                                                                                                                              356 GIGITIGCIGCITGIGIAGGCITIGGIAIGGGCITITATTIGCTICTGGAIGITIGIGI
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                                                                                                                                                                                                                                                                                   Sequence 458 BP; 80 A; 115 C; 149 G; 114 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 ACTACTIGGGITIGITICAATTATTATGAGCAGTIGCGTATIGI
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                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADX50588 standard; cDNA; 1216
                                                                                                                                                                                                                                                                                                                    84.6%;
98.6%;
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05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.6'
Matches 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein content; gene; ss
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                                                                                                                                                                                                                                               invention
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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the sequence. The recombination of the polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, cecombination in plants, for improving yield by modification of photosynthesis or carbohydrate, introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one strong content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert of the increase.
                                                                                                                                                                                                 New recombinant DNA construct, useful for improving plant tolerance to ocld, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                         Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1216 BP; 282 A; 342 C; 402 G; 190 T; 0 U; 0 Other;
                                                                                                                         Tabaska JE,
                                                                                                                       Screen SE,
                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 25328; 15pp; English
                                                                                                                     Zhou Y, Kovalic DK,
ZHOU Y.
KOVALIC D K.
SCREEN S E.
                                                       TABASKA J E. CAO Y.
                                                                                                                                                              WPI; 2004-180133/17.
                      (KOVA/) H
(SCRE/) S
(TABA/) T
(CAOY/) C
      (ZHOU/)
                                                                                                                       Liu J,
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Gaps ö DB 13; Length 1216; Indels 4; 84.6%; Score 278.4; DB 13 98.6%; Pred. No. 4.4e-75; iive 0; Mismatches 4; Best Local Similarity 98.6 Matches 279; Conservative Query Match

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993

1114 GIGITGCTGCTGTGTAGGCTTTGGTACGTATGGCTTTATTTGCTTCTGGATGTTGTGT 1173 1054 caadgrogarcccrogroaagrocgrogrorrraaagacccaccccccroccacrogroa 1113 121 CAAGGTGGATCGCGTGGTCAAGGCCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA 180 181 GTGTTGCTGCTTGTGTAGGCTTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT 240 셤 ò ò g ઠ

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Search completed: March 8, 2006, 04:18:51 Job time : 386.692 secs

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BV106713 PZA01565
BV10679991 scl186 p5
BV106709 PZA01565
BV106709 PZA01565
BV1067098 scl186 p5
BV106715 PZA01565
BV106712 PZA01565
BV106712 PZA01565
BV106712 PZA01565
BV106717 PZA01565
BV106717 PZA01565
BV106717 PZA01565
BV106717 PZA01565
AC115865 MVB mWBCU
AC11548 REATURE NO
AC11548 PMUB mWBCU
AC11589 MWB mWBCU
AC11589 MWB mWBCU
AC151829 MWB mWBCU
AC163716 PMU FCOGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dakker, H.A., Florack, D.E. and Bosch, H.J.
Gntii (udp-n-acetylglucosamine:beta-d mannoside
beta(1,4)-n-acetylglucosaminyltransferase iii) expression in plants
Patent: WO 03078614-A 10 25-SEP-2003;
Plant Research International B.V. (NL)
Location/Qualifiers
1. 7545
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7545;
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Pred. No. 2.6e-82;
); Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7545 bp I Sequence 10 from Patent WO03078614. AX840288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                             ACII5865
ACI37970
ACI37970
ACI3521
ACI3537
ACI41091
ACO19402
ACI51829
ACI51829
ACI39885
ACI39885
ACI39885
ACI39885
ACI372716
                                                                                                                       BV079988
BV106715
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BV106712
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BV106717
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AC115865
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Matches 329; Conservative
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synthetic construct
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Best Local Similarity
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13.0
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BD272351 Root-spec
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1041 CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTAAAAGACCCACCGGCACTCGCAGTGA 1100
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GEHKCHFPPAPAPPPHVETHHPVVVHKI EDDDTKTQTPPQAPEEEKKGLLDKI KEKLPG
GHKKPEDAAAAAAAAAAPAVHAPPPPAPHAEVDVSSPDGKKGLLGKIMDKI PGYHKSSGEE
DRKDAAGEHKTSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MEDERNTQQHQGGEQAQDQENEVKDRGLLDSLLGRNKHDDQEKK
NQQEEEELATGMEKVTVAEPDHKEEGHEAAEKKDSLLAKLHRTSSSSSSSSDDEEEEV
          Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bormatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 1277)
Pack,N.C., Taylor,B.H., Magill,C.W., Cobb,B.G. and Smith,J.D. Induction of embryo quiescence in developing maize kernels is Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to barley dehydrin-8 and wheat cold-acclimation protein WCOR410"
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/tissue_type="scutellum"
/do_tze_type="3-day-old germinating seed"
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'note="drought-inducible gene'
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/product="dehydrin"
/protein_id="AAA33480.1"
/db_xref="GI:532623"
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/organism="Zea mays"
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/strain="TX5855"
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Gntiii (udp-n-acetylglucosamine:beta-d mannoside
betalt,4)-n-acetylglucosaminyltransferase iii) expression in plants
Patent: WO 03078614-11 25-SEP-2003;
Plant Research International B.V. (NL)
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Zea mays dehydrin (dhn-2) mRNA, complete cds.
L38913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 329; DB 6;
Pred. No. 2.7e-82;
0; Mismatches 3;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_type="taxon:32630"
/note="Synthetic"
                                                                                                                                                                        redacarrerrargrarraaraarrecrrrec 7704
                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                TGGACATTGTTATGTATTAATAAATGCTTTGC 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                     other sequences; artificial sequences
                                                                                                                                                                                                                                                                                  Sequence 11 from Patent WO03078614. AX840289
                                                                                                                                                                                                                                                                                                                                                      AX840289.1 GI:39978688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.1%; E
Matches 329; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct
synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L35913.1 GI:532622
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source

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                            AAGGCCCGTGTGTTTA----AANACCCACCGGCACTGGCAGTGAGTGTTGCTGCTTG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (Dases 1 to 1333)

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                                                                                                                                                                                                                        82 GTGTGCTTCTGGTTTGCTTTAATTTTACC--AAGTTTGTTTCAAGGTGGATCGCGTGGTC
                                                                                                                                                                                                                                                                                                    TGTTGTGTACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCT
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ROOF-specific promoter

L Patent: JP 200233760-A 1 12-NOV-2002;

ADVANTA TECHNOLOGY LTD

OS Zea mays (maize)

PD 12-NOV-2002

PP 16-NOV-1998 JP 2000582576

PT SUSAN ELY.IAN JEFFREY EVANS, WOLFGANG WALTER SCHUCH PC C12M15/09, C12M5/09, C1
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           83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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           Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
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Root-specific promoter.
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JP 2002537760-A/1.
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           Conservative
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Matches 211; Conserv
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Zea mays
           211;
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           Matches
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AUTHORS
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BD272350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-2004) Waksman Institute, Rutgers University, 190
Frelinghuysen Rd, Piscataway, NJ 08854, USA
Location/Qualifiers
1. 722
/organism="Zea mays"
/mol_type="mana"
/db &ref="tanna"
/clone="Contig566.P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             530 CAAGGTGGATCGCGTGGTCAAGGTCCGTGTGTTTAAAGACCCACCGGCACTGGCAGTGA 589
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                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 722)

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Characterization of the maize endosperm transcriptome and its comparison to the rice genome
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTTGCTGCTTGTGTAGGCTTTTGGTACGTATGGGCTTTTATTTGCTTCTGGATGTTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 722)
Lai,J., Dey,N., Kim,C.-S., Bharti,A.K., Rudd,S., Mayer,K.F.X.,
Larkins,B., Becraft,P. and Messing,J.
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Pred. No. 9.5e-15;
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Unclassified.
Unclassified.
1 (bases 1 to 1333)
Ely,S., Evans,I.Jeffrey. and Schuch,W.Walter.
Root-specific promoter
Root-specific promoter
Patent: US 5837848-A 1 17-NOV-1998;
Location/Qualifiers
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/wol_type="unassigned DNA"
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AR059010 GI:5984587
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64.7%;
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Matches 294; Conservative
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PAT 17-JUL-2003

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Exergota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicodidae; Panicodidae; Panicodidae; Panicodidae; Panicodidae; Panicodidae; Panicodidae; Li (Dases 1 to 758)

Ely,S., Evans,I.J. and Schuch,W.W.

Root-specific promocer

ADVANT: TECHNOLOGY LTD
OS Zed mays (maize)
PN 12-002537760-A/2
PN 12-NOV-2002
PN 12-NOV-2002
PN 12-NOV-1998 JP 2000582576
PI SUSAN ELY,IAN JEFFREY EVANS,WOLFGANG WALTER SCHUCH PC CL2NIS/09,CL2NS/10/A01HS/00,CL2NIS/00,CL2NIS/10/A01HS/00,CL2NIS/00,CL2NIS/10/A01HS/00,CL2NIS/09 CC a, c, t, g, other or unknown
FM Key
FT modified base (429)
FT modified base (480)
FT modified—base (480)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 ATTAAGGTGGATCGCGTGACTCTGGCAGTGTTGCTGCTTGTGTAGGACGTGGTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 GGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACCTGGA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 291)
Lalgudi,R.V., Ito,L.Y. and Sherman,B.K.
Polymucleotides and polypeptides derived from corn ear
Patent: US 6476212-A 6335 05-NOV-2002;
Incyte Genomics, Inc.; Palo Alto, CA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 758;
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Sequence 6335 from patent US 6476212.
AR250976.1 GI:27298850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:4577"
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/mol_type="genomic DNA"
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Location/Qualifiers
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Best Local Similarity 68.2°
Matches 202; Conservative
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AR250976
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1055 TGTGTGTTGGGTTTGGTTTGCCTAAAGTTTGTTTCAAGGTGGATCGCCTGGTC 1114
                                                                                                           AAGGICCGIGIGCICTATIAAGGIGGATCGCGIGACICTGGCAGIGAGIGTIGCTGCTIG 1174
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                                                                   AAGGCCCGTGTGCTTTA----AANACCCACCGGCACTGGCAGTGAGTGTTGCTTG
                                                                                                                                                                                                                                           233 TGTTGTGTACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 CITIAATITIACC--AAGITIGITICAAGGIGGAICGCGGGGTCAAGGCCCGIGIGCTIT
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                                                                                                                                                        TGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTGGA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown.
Unclassified.
1 (bases 1 to 758)
1Sly.S., Evans, I.Jeffrey. and Schuch, W.Walter.
Root-specific promoter
Patent: US 5837848-A 2 17-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.8%; Score 84.8; DB 6; 68.2%; Pred. No. 5.3e-13; iive 0; Mismatches 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AR059011 758 bp
Sequence 2 from patent US 5837848.
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                                                                                                                                                                                                                                                                                                                                GGGCTACCTGGACATTGTTATGTATT 318
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Root-specific promoter.
BD272351
BD272351.1 GI:33082119
JP 2002537760-A/2.
Zea mays
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Best Local Similarity 68.2
Matches 202; Conservative
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'organism="Zea mays"
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                                                                                                                                                                 Query Match 22.1%;
Best Local.Similarity 67.1%;
Matches 141; Conservative
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Zea mays
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BV106706
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                                                                                                                                                96 IGCTITAAITITACCAAGITITGTITCAAGGIGGAICGCGIGGICAAGGCCCGIGIGCTIT 155
                                                                                                                    128 rdcir---rraccaaaagririciricaaggricacciogricaaggriccordicaa
                                                                                                                                                                                                             156 AAANACCCACCGGC---ACTGGCAGTGAGTGTTGCTGCTTGTGTAGGCTTTTGGTACGTAT 212
                                                                                                                                                                                                                              Zea mays
Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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43 60 59
88 82 79
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McMullen,M.D., Vrob Bi,I., Schroeder,S.S. and Gaut,B.S. MPZ-UCI Joint SNP Discovery Unpublished (2003)
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplifag DNA polymerase
Sequence ran on ABI 3700 sequencer.
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                             Length 291;
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74 74
90 90
                                                          Indels
                                                                                       38 GGCCGGCCCTTGGCCGCGCGATCAGAANCGTTGCGTTGGCGTGTGTGTGT
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U.C. Irvine
121 Schinbaus Hall, Irvine, CA 92697-2525, USA
122 Schinbaus Hall, Irvine, CA 92697-2525, USA
Pax: (949) 824-2181
Email: Dgautdwoil.edu
Erimer A: ACCDANAGTTTGTTTCTTGA
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50
84
                            Score 76.6; DB 6; 1
Pred. No. 1.1e-10; 0; Mismatches 36;
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PCR amplification of genomic DNA
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each 0.5 uM
dWTPs:
Taq Polymerase: Redraq (Sigma)
Total Vol:
plicon sowner.
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BV079994.1 GI:37051651
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Sequencing buffer
d-Rhodamine kit (ABI)
                             23.3%;
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                          Query Match
23.34
Best Local Similarity 76.44
Matches 146; Conservative
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TITLE
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BV079994
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BV106706
PZA01565 B73(2) Zea mays B73(2) Zea mays STS genomic, sequence
tagged site.
BV106706
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                   TTGTTTCAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGC---AC
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                                                     /db_xref="taxon:4577"
/clone_lib="zea mays Ky21"
/dev_stage="seedling"
/note="organ: leaf; genomic DNA from inbred line"
<1. .>233
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ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplifaq DNA polymerase
Sequence ran on ABI 3700 sequencer.
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                                                                                                                                                                                                                                                                 Length 233;
                                                                                                                                                                                                                                                              Score 72.8; DB 10; Length;
Pred. No. 1.3e-09;
0; Mismatches 49; Indels
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U.C. Irvine
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Fax: (949) 824-2564
Email: bgautôwci.edu
Primer A: ACCAAAAGTTTCTTTCAAGGTGA
Primer B: TTTTTGGGCAGAAACC
STS. 84%: 233
/mol_type="genomic DNA"
/cultivar="Ky21"
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Total Vol: 10 ul
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each 200 uM
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BV079992.1 GI:37051649
 Email: bgaut@uci.edu
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                                                                                                                            dNTPs:
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BV079992
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genomic, sequence tagged
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Pred. No. 1.3e-09;
0; Mismatches 49; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4577"
/clone_lib="Zea mays B73(2)"
/dev_stage="seedling"
/note=organ: leaf; genomic DNA from inbred line"
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MCMullen, M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Fax: (949) 824-2564
Fax: (949) 824-2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BV106711 233 bp DNA PZA01565 Ky21 Zea mays STS
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                                                                                                                                                                                                                                                                                  organism="Zea mays"
mol type="genomic DNA"
cultivar="B73(2)"
Genomic DNA amplification
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                             Sequencing buffer
d-Rhodamine kit (ABI)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.1%;
Best Local Similarity 67.1%;
Matches 141; Conservative
              RedTaq (Sigma
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BV106711.1
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VERSION
KEYWORDS
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ORGANISM
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TITLE
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COMMENT
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STS 30-SEP-2003
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/clone_lib="Zea mays Ky21"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
/10.0="Organ: leaf; genomic DNA from inbred line"
                                                                                                                                                                                                                                   ABI protocol - using d-Rhodamine terminator cycle sequencing ready reaction with amplifaq DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.1%; Score 72.8; DB 10; Length 233; 67.1%; Pred. No. 1.3e-09;
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Primer A: ACCAAAGTTTGTTTCAAGGTGGA
Primer B: TTTTTGGGCAGAAACCAAAGC
STS size: 233
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
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/cultivar="Ky21"
                                                                                                                                                                          Tag Polymerase: RedTag (Sigma)
Total Vol: 10 ul
                                                                                                                            each 0.5 uM
each 200 uM
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RedTaq (Sigma)
Sequencing buffer
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ABI protocol - usi
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3V106708 237 bp DNA linear STS 13-MAR-2004
PZA01565 Ill4H Zea mays Ill4H Zea mays STS genomic, sequence tagged
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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sequencing ready reaction with amplifaq DNA polymerase
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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.ed
Primer A: ACCAAAAGTTTGTTTCAAGGTGGA
Primer B: TTTTTGGGCAGAAACCAAAGC
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Template: 50 ng
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Total Vol:
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each 200 uM
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Redrag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
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BV106708.1
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Zea mays
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                                                                                    RESULT 14
BV106708
LOCUS
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                                                                                                                  Eukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Beprantophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoidae, Andropogoneae, Zea.

(bases 1 to 237)

(bases 1 to 237)

MPZ-UCI Joint SNP Discovery
Unpublished (2003)
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/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .-237
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sequencing ready reaction with amplifaq DNA polymerase
Sequence ran on ABI 3700 sequencer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 GCAGCTGCGTGTTGTAATTCGGCTGGGCTACCCTGGATGCGTTAATAATT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72.4; DB 10; Length 237;
Pred. No. 1.7e-09;
0; Mismatches 43; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Donted: Brainway of Sautenary Biology U.C. Irvine Broingay and Evolutionary Biology U.C. Irvine Brain (1949) 824-254 Fax: (949) 824-2581 Email: Byaufouci.edu Email: Byaufouci.edu Erimer A: ACCAAAAGTTTGTTTCAAGGTGGA Primer B: TTTTTGGGCAGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protocol:
PCR amplification of genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dNTPs:
each 0.5 uM
dNTPs:
each 200 uM
Taq Polymerase: RedTaq (Sigma)
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nlice control of the control of
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/mol_type="genomic DNA"
/cultivar="Il14H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:4577"
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Redrag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Brandon S. Gaut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.0%;
68.3%;
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Matches 157; Conservative
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                                              Zea mays
                                                                                         Zea mays
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Search completed: March 8, 2006, 06:32:08 Job time: 2384.09 secs
 cultivar="B73"
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scll86_p5 B73 Zea mays B73 Zea mays STS genomic, sequence tagged
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1 (bases 1 to 232)

McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.

MPZ-UGI Joint SNP Discovery
Unpublished (2003)
                                                                                                                170 ACTGGCAGTGAGTGTTGCTTGCTTGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCT 229
                                                                                                                                    230 GGA-------TGTTGTGTACTTGGGTTTGTTGAATTATTATGA 268
                                                                                                                                                                                                   9
                                                                    1 IGITICAAGGIGGATCGCCTCGTCAAGGTCCCTGTGTGCTCTATTAAGGTGGATCGCGTGAC
                                                   116 TGTTTCAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANAC-----CCACCGGC
                  Gaps
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sequencing ready reaction with amplifag DNA polymerase
Sequence ran on ABI 3700 sequencer.
                                                                                                                                                                                                                                              30;
                  43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACCAAAAGTTTCTTCAAGGTGGA
 Pred. No. 1.7e-09;
0; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protocol:
PCR amplification of genomic DNA
Template: 50 ng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dNTPs: each 0.5 uM dNTPs: each 200 uM Taq Polymerase: RedTaq (Sigma) Total VO::
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Redrag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
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BV079989.1 GI:37051646
68.38;
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                  Matches 157; Conservative
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                 RESULT 15
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/organism≃"Zea mays" /mol_type="genomic DNA"

source

FEATURES

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3
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                                                                                                                                                                                                                                                         174 GCAGIGAGIGITGCIGCITGIGIAGGCITTGGIACGIAIGGCITTAITTGCTICTGGAI 233
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                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                 117 GTTTCAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCAC---CGGCACTG
                                                                                                                                                                                                                                                                                                                                234 GITGIGIACTACTIGGGITTG------TIGAATTATTATGANCAGTIGC
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                                                                                                                                                          Gaps
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/clone_lib="Zea mays B73"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. >>232
                                                                                                                                                          20;
                                                                                                                       Length
                                                                                                                                                         49; Indels
                                                                                                                     Score 70.8; DB 10;
Pred. No. 4.8e-09;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                   277 GTATTGTAATTCAGCTGGGCTACCTGGA 304
                                                                                                                        21.5%;
66.8%;
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Matches 139; Conservative
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FEATURES
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MEST867 H
MEST840 H
EST6709 Z
zmrw805 0
zmrw848 0
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603005B09
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CF628060 zmrws48_0
AI629748 486035A08
CF629847 zmrws48_0
                                                                     March 8, 2006, 04:07:00; Search time 2667.19 Seconds (without alignments) 5823.847 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                 1 ggtcgcagcgtgtgcgtgtc......tgtattaataaatgctttgc 332
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A1649488
DN212434
DN212434
DN212434
DN212434
CCC00159
CCR27377
CCK327377
CCK32415
CCK34415
CCK34415
CCK34415
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CB380909
DN232860
DN232769
DN828411
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                             41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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329
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Match Length DB
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gb_est2:*
gb_htc::*
gb_est4:*
gb_est6:*
gb_est6:*
gb_est7:*
gb_gss2:*
gb_gss2:*
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                                                                                                                                      Perfect score:
                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                   Sequence:
                                                                                                                                                                                                             Searched:
                                                                        Run on:
                                                                                                                         Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
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Location/Qualifiers
1. 519
/organism="Zea mays"
/mol_type="mRNA"
/cultivare="B73"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGTTGCTGCTTGTAGGCTTTGGTACGTATGGCCTTTATTTTGCTTCTGGATGTTGTGT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                            /clone_lib="ISUMG"
/note="Vector: pSlip7 (4.43 kb); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 CAAGGTGGATCGCGTGGTCAAGGTCCGTGTGTTAAAGACCCACCGGCACTGGCAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 ACTACTIGGGTITGTIGAATTATTATGAGCAGTIGCGTATTGTAATTCAGCTGGCTACC
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/clone="MEST543-E03"
/tissue_type="mixed"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local S:
Matches 328
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BM381414 15-JAN-2002 mRNA linear EST 16-JAN-2002 MEST534-E06.univ ISUM6 Zea mays cDNA clone MEST534-E06 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: schnable@lastate.edu
Individual basecall and confidence value were assigned using the
Individual basecall and confidence value were assigned using the
bred software (http://www.phrap.org/). Overall sequence quality
assessment and vector trimming was conducted using the bucy
software (version 1.16s, http://www.tigr.org/softlab/). Lucy
parameters were set to ensure an overall trimmed quality of 97.5$
or better without any vector fragments in the chosen high quality
region of each sequence. Low-quality bases between the poly-T and
the high-quality region were replaced with N's to serve as spacers
using a Perl program (est_process.pl), written by Dr. Hui-Hsien
                                                                                                                                                                                                                                                                       Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones Unpublished (2001)
                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                            Contact: Patrick S. Schnable Schnable Laboratory Iowa State University 2015B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA Pax: 515-294-6975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer Sp6 (ATT TAG GTG ACA CTA TAG)
Seg primer: universal (GTA AAA CGA CGG CCA GT)
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                           GI:18180204
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BM381414/c
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TITLE
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acid)-treated seedlings; GATGCC--Kinetin-treated seedlings; AAGACC--ACPC (1-aminocyclopropane-1-carboxylix acid)-treated seedlings; GCCTGA--Brassinolide-treated seedlings; GCTGA-BA (Abbacisic acid)-treated seedlings; TACGGA--GA (Gibberellic acid)-treated seedlings; TACGGA--GA (Gamonic acid)-treated seedlings; Equal amounts of first-strand cDNA from each reaction were combined and used as template for DNA PolI-catalyzed 2nd strand synthesis. After the addition of EcoRI adaptors, ds-CDNAs were disectionally cloned into the EcoRI and NotI sites of the pSlip7 expression vector. Plasmid DNA isolated from the library was digested with NotI to remove the treated from the library was digested with NotI to remove the treated from the library was digested with NotI to remove the treated from the library was digested with NotI to remove the treated from the library was digested with NotI to remove the treated from the library was digested with NotI to remove the treated from the library was digested with NotI to remove the treated from the library was digested with NotI to remove the treated from the library was digested with NotI to remove the treated from the library was digested with NotI to remove the treated from the library was manner from the library was digested.
                                                                                                                                                                                                                                                                                                                                                                                                                                              empty vector clones. Linear DNAs from 5.4 to 7 kb were gol
purified and ligated at low concentration to promote
recircularization. Ligation products were precipitated and
transformed into DHIOB host cells. The complexity of the
resulting library was 1.2 x 10X6."
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 615)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 99.5%; Score 327.4; DB 3; Length 559; Il Similarity 98.8%; Pred. No. 6.5e-82; 328; Conservative 0; Mismatches 4; Indels 0
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Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fat: 650 723 2227
Fax: 650 725 8221
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UNZ04249 615 bp mRNA linear EST 28-FEB-2005
MEST801 F08.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
DNZ04249
                                                                                                                                                                                                                                                           /note="Organ: root; Vector: pBluescriptII SK(+) XR;
Seedling stressed root cDNA library from Wang/Bohnert lab"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen, H.D., Zhang, X., Zhou, R.L., Arias L, A.C., Shendelman, J.M., Zazubovits, N., Borsuk, L.A., Emrich, S.J., Ashlock, D.A., Scanlon, M.J. and Schnable, P.S.
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clade; Panicoideae; Andropogoneae; Zea.
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Unpublished (2004)
                                                                                                                                     db_xref="taxon:4577"
/tissue_type="seedling"
/dev_stage="salt_stress"
/lab_host="B. coli XL Gold"
/clone_lib="603 - stressed root cDNA library from Wang/Bohnert lab"
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203B R.J. carver Co-Lab, Ames, IA 50011-3650, USA
TH1: 515-294-0975
Fax: 515-294-5256
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                                                                            /organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
                      3005 row: B colum
Location/Qualifiers
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Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: schnable@iastate.edu.
Location/Qualifiers
1. 615
  walbot@stanford.edu
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Email: walbot@
Plate: 603005
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DEFINITION

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in SOLK cells and plated onto LB-ampicillin agar plates.

Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria.

(-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove B. coll, vector, and organelle contamination. After processing -30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."
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                                      db_xref="taxon:4577"
rtissue type="vegetative Shoot Apical Meristem (SAM) and
teaf prImordia staged P1-P4"
lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 GTGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGCTTTATTTGCTTCTGGATGTTGTGT
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mol_type="mRNA"
cultivar="inbred B73"
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Best Local Similarity 98.8
Matches 328; Conservative
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linear

mRNA

dq 099

CF629927

RESULT 5 CF629927/c LOCUS

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/clone lib="armwagh"/
/clone lib armwagh lib after transplanted to high
/clone lib armwagh lib after transplanting. About
libraries (zmrws05 and zmrws48) while 500 roots were
combined from each of the two time points at high water
potential (zmrww00). Each root was divided into 4 segments
/cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7
mm; segment 1, 0-3 mm plus the root cap; segment 2, 3-7
mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details
of conditions see (1) with nutrient modifications as in
(2). The three normalized cDNA libraries were constructed
in the lab of Hans Dehnert (University of Illinois-UC).
Total RNA was extracted by the 'hot Phenol' method (Plant
Molecular Biology mannal. Ds: -13, 2nd ed., 1997). This
method worked in eliminating carbohydrate material present
in the root tips. The integrity of the RNA was verified by
denaturing agarose gels and spectrophotometry (ratio Adenaturing 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was converted to domine benamed the was converted to deferent segment of the root was added to the 3 -end of the modified Oligo(dT) primers, including a Not1 site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix ($1, $2, $3, or $4$) has been added to each sequence identifier to designate which region of the root (Root_segment_1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of so indicates that the sequence tag, and hence the source segment, could not be identified. The double strander cDNAs were size-selected ($450 bp). Size selected cDNAs were adaptored with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(*) pagemid vector (Stratagene) and electroporated into E.coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrws05: 3.37 x 106; zmrws06: 3 x 206; zmrws06: 3 x 206. The background of empty clones was less than 1%.
                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 660)
Bohnert, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredricksen, M., Sharp, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A., Topinka, C., Davis, G.E., Schachtman, D., Wu, Y. and Nguyen, H.T. NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root Unpublished (2003)
                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea..
zmrws48 0A20-006-h12.s3 zmrws48 Zea mays cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Pax: 217-333-5574
Email: bohnerth@life.uiuc.edu
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PURS. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for smplification using the T7 and T3 priming sites that flank the cloned circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C. Non-hybridized BNA endered DNA circles were separated from hybridized BNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: znrw805: 2.0x107; zmrw846; 4.2x107; zmrw800: 1.1x107. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R B; Silk W K; Hsiao T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50.57. (2) Spollen W G; LeNoble M E; Samuels T D; Bernstein N; Sharp R E. Abscisic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March, 2000. 967-976.
TAG SEO-FCGCA.
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TAG_SEQ=TCGCA"
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339 dercechecererecererecerecerereneseeceeceecereeeceeces Gaps ö Length 660; Indela DB 6; 4 Score 327.4; DB 6; Pred. No. 6.7e-82; 0; Mismatches 4; 99.5%; Conservative Query Match Best Local Similarity Matches 328; Conserv 61 셤 ð

ORIGIN

160 240 GIGTTGCTGCTTGTTGGTAGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT 100 241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300 40 219 CAAGGTGGATCGCGTGGTCGAAGGTCCGTGTTTAAAGACCCCACCGGCACTGGAGGA 99 ACTACTTGGGTTTGTTGAATTATTATGAGCAGTTGCGTATTGTAATTCAGCTGGGTACC 121 CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA GTGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT 159 181 원 ઠે 셤 ò 셤 ò 셤

DN212434 675 bp mRNA linear EST 28-FE MEST940 E08.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence. DN212434 DN212434.1 GI:60345461 Zea mays **Zea** mays DEFINITION ACCESSION KEYWORDS SOURCE ORGANISM DN212434/c VERSION

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases I to 675)

Chen, H.D., Zhang, X., Zhou, R.L., Arias L, A.C., Shendelman, J.M., Zazubovits, N., Borsuk, L.A., Emrich, S.J., Ashlock, D.A., Scanlon, M.J. and Schnable, P.S.

REFERENCE AUTHORS

Sequence Tags from B73 Maize Shoot Apical Meristems USA Contact: Patrick S. Schnable Schnable Laboratory Iowa State University 2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, Tel: 515-294-0975 Fax: 515-294-5256 Email: schnable@iastate.edu. /mol_type="mRNA" /cultivar="inbred B73" 'organism="Zea mays" Location/Qualifiers source

Gaps ; 0 Length 675; 4; Indels Score 327.4; DB 8; Pred. No. 6.8e-82; 0; Mismatches 4; 99.5%; Matches 328; Conservative Best Local Similarity Query Match

ORIGIN

TGGACATTGTTATGTATTAATAATGCTTTGC 332 TGGACATTGTTATGTATTAATAAATGCTTTGC 8

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180 299 120 239 238 CAAGGTGGATCGCGTGGTCAAGGTCCGTGTGCTTTAAAGACCCACCGGCACTGGCAGTGA 179 CAAGGTGGATCGCGTGGTCAAGGCCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA 358 121 ઠે 셤 8 a Š g

240 GIGTTGCTGCTTGTAGGCTTTGGTACGTATGGGCTTTATTTTGCTTCTGGATGTTGTGT GTGTTGCTGCTTGTGTAGGCTTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT 181 178

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TITLE JOURNAL COMMENT

AUTHORS REFERENCE

DR955206/c DEFINITION

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CC700159 782 bp DNA linear GSS 19-JUN-2003 OGUEI01TH ZM_0.7_1.5_KB Zea mays genomic clone ZMVBMa0421A01,
                                                                                                                                              241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw (C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUBI01Ty
                                                                                                                                                                                                                                          100 ACTACTTGGGTTTGTTGAATTATTATGAGCAGTTGCGTATTGTAATTCAGCTGGGTACC
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Tel: 301-838-5843
     Pred. No. 6.9e-82;
0; Mismatches 4;
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Class: methylation filtered.
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     Best Local Similarity 98.8%;
Matches 328; Conservative
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/woltype="mRNA"
/culfivaz="877"
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tips, leaf, root tips, whole seed, embryo)"
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NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of EMRNA with a 5 cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources: Tissues prepared! 1 just emerging sitks; 2. inner husks from ears of sample #1; 3.20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5.2 mm to 2 cm ears; 6. pollen; 7.1 cm vegetarive shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9.0.5 cm long root tips from 15 day old seedlings; 10.10 dap whole seed; 11.12 dap endosperm and embryo. 12.17 dap endosperm and embryo. 13.1.12 dap endosperm archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona. Clones, high the the University of Arizona. Clones to the Arizona clones of the Arizona clones in Maize mandembryo. Illores and seeding and amplified library can be ordered from the University of Arizona. Clones of the Arizona clones of the
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clade, Panicoideae, Andropogoneae, Zea.
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Kim.H., Collura.K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller.K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
DR955206 753 bp mRNA linear EST
ZM_BFb0049D21.f ZM_BFb Zea mays cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
121 520 626 9585
Fax: 520 621 1259
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Plate: 0049 row: D column: 21.
Location/Qualifiers
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Arizona Genomics Institute
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1 (basea I to 444)
Yang, H. and McCormick, S.
Transcriptome of Zea mays embryo sac
Unpublished (2004)
Contact: Yang, H.; McCormick, S.
Plant Gene Expression Center
                                                                                        CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA 180
                                                                                                                      437 CAAGGIGGAICGCGIGGICAAGGICCGIGIGCTITIAAAGACCCACCGGCACTGGCAGIGA 378
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                                                           GGTCGCAGCGTGTCCGTCGTACGTTCTGGCCGGCCGGGCCTTGGGCCGCCGATC
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isolated with enzymatic maceration and manual
microdissection. RNA was extracted from the embryo
CDNA library was constructed by oligo dT priming us
directionally cloned."
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Tel: 510 559 5906
Fax: 510 559 5678
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Location/Qualifiers
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/done lib-"amrenubl library was created by subtracting the water-targeted maize root library amwwwoof from the water-starved maize root library amwwwoof from the water-starved maize root library amwwwoof from the water-starved maize root libraries zmrwwoof and zmrwas9.

The 3 starting libraries are described below in (3).

Purified plasmid preps from zmrwas05 and zmrwas98 were combined. Sequenced clones from the zmrwwool library were pooled and converted into single-stranded circles and used as a driver for subtraction. The PCR products from the driver were hybridized with the single-stranded version of the zmrws05-zmrws48 library for 88 hours at 30 oC. Unhybridized single-stranded DNA circles were separated from hybridized blank rendered partially double-stranded and electroporated into DH1108 cells to generate the subtracted library. The total number of clones was 2 x 106 cfu. Background of empty clones (detected by blue/white selection on agar places) was approximately 10%. Insert size of the subtracted library, determined by PCR of the entire library, ranges from 0.5 to 2.1kb). (3) Root samples were collected in Robert E. Sharp's lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CK827377 603 bp mRNA linear BST 03-MAR-2004
zmrsubl 0B20-006-a09.s0 zmrsubl Zea mays cDNA 3', mRNA sequence.
CK827377
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Bohnert, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredricksen, M., Sharp, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A., Topinka, C., Davis, G.E., Schachtman, D., Wu, Y. and Nguyen, H.T. NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root Unpublished (2003)
                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                            CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA
196 CAAGGTGGATCGCGTGGTCAAGGTCCGTGTGCTTTAAAGACCCACCGGCACTGGCGGTGA
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University of Illinois, Urbana-Champaign
University of Illinois, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohnerth@life.uiuc.edu
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/mol_type="mRNA"
/db_xref="taxon:4577"
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Indels

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Mismatches

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Matches 327; Conservative

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CF633415 412 bp mRNA linear EST 02-OCT-2003
Zmrws48 0B20-015-£03.s3 zmrws48 Zea mays CDNA 3', mRNA sequence.
CF633415
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Bohnert, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredricksen, M., Sharp, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A., Topinka, C., Davis, G.E., Schachtman, D., Wu, Y. and Nguyen, H.T. NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root Signaling Under Drought
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA
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Tel: 217-265-5475
Fax: 217-333-5574
Email: bohnerth@life.uiuc.edu
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/db xref="taxon:4577"
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(2)). The three normalized CDNA libraries were constructed for the lab of fams bonner (University of Illinois 10.7). The total RNA was extracted by the 'hor Phenol' method (Plant Molecular Biology manual DS: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tipe. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio Aso/280). Poly(A)-mRNA was isolated bytice from total RNA using the Oligotex Direct mRNA kas isolated bytice from total RNA was converted to double-stranded CDNA and tagged by using modified Oligo(dT) primers. One of a sequence tagged by using corresponding to a different segment of the root was added to the 3'-end of the amdilied Oligo(dT) primers. One of a sequence tagged by using a Not! site and used to reverse transcribe the segment-specific mRNAs into CDNAs. Bach library contains all four tags. A suffix (sl., sJ., sJ., or s), the sequence was found in based on the Identification of the tagged by using the root (Root geoment; 2, 3, or 4), the sequence was found in based on the Identification of the tagger of the root of so indicates that the sequence tagger The Contain Manual CONDAS were adaptored with Rol! The CDNAs were adaptored with Econi adaptors at both ends, and then digested with No!! The CDNAs was as follows: rarned CDNAs were adaptored with Econi adaptors at both ends, ince ECONI World digested pBS II SK(+) phagemid vector (ctal number of white colony forming units (cfu) in the transvelo; 3.37 x 105; zmrws61: 487 x 106; zmrws61: zmr

ö 221 180 220 CAAGGTGGATCGCGTGGTCAGGTCCGTGTGCTTTAAAGACCCACCGGCACTGGCAGTGA 161 121 CAAGGIGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA Gaps ö Length 412; Indels Score 324.2; DB 6; Pred. No. 5e-81; 0; Mismatches 6; . Query Match 98.5%; Best Local Similarity 98.2%; Matches 326; Conservative ORIGIN g 셤 Š ठ ò

8512236 Zea mays embryo sac cDNA library Zea mays cDNA clone BS5242 CN844286 /clone_lib="Zea mays embryo sac cDNA library"
hote="Vector: Clontech Triplex2; Embryo sacs were
isolated with enzymatic maceration and manual
microdissection. RNA was extracted from the embryo sacs. A
cond library was constructed by oligo dT priming using the
Clontech SMART cDNA synthesis kit. The cDNAs were
directionally cloned." ö 180 160 GTGTTGCTGCTTGTGTAGGCTTTGGTATGGCCTTTATTTGCTTCTGGATGTTGTGT 101 241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300 76 Gercecaecererecerereceracerrerececeeceecesecerreseces 120 136 AGAAGCGTTGCGTTGGCGTGTGTGTGCTTTCTGGNTTGCTTTAATTTTACCAAGTTTGTTT 195 CAAGGTGGATCGCGTGGTCAAGGTCCGTGTGCTTTAAAGACCCACCGGCACTGGCGGTGA 255 | GTGTTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT 240 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. 100 ACTACTTGGGTTTGTTGAATTATTATGAGCAGTTGCGTATTGTAATTCAGCTGGGCTACC 41 9 CAAGGTGGATCGCGTGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA GTGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT Gaps ö Length 443; IndelB 6 DB 7; Score 321.8; DB 7 Pred. No. 2.4e-80; 0; Mismatches 9 800 Buchanan St. Albany, CA 94710, USA Tel: 510 559 5906
Fax: 510 559 5678
Email: shellam@mature.berkeley.edu.
Location/Qualifiers 301 TGGACATTGTTATGTATAATAATGCTTTGC 332 40 TGGACATTGTTATGTATTAATAAATGCTAAGC 9 1 (bases 1 to 443)
Yang, H. and McCormick, S.
Transcriptome of Zea mays embryo sac
Unpublished (2004) S. cell type="embryo sac" /db_xref="taxon:4577" /clone="ES5242" Contact: Yang, H.; McCormick, Plant Gene Expression Center organism="Zea mays" /mol_type="mRNA" /cultivar="A188" CN844286.1 GI:47961577 97.8%; Query Match Best Local Similarity 97.3 Matches 323; Conservative . . 443 Zea mays Zea mays USDA/ARS 19 121 196 181 181 source DEFINITION ORGANISM TITLE JOURNAL COMMENT ACCESSION RESULT 12 CN844286 VERSION KEYWORDS SOURCE AUTHORS REFERENCE FEATURES ORIGIN 8 ò g ઠે 셤 ઠ 셤 ઠ d ઠ 셤 Š

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MEST19-A06.T3 ISUM4-TN Zea mays cDNA clone MEST19-A06 3', mRNA
                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (basea) 1 to 434)
Qlu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14207545.
Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 GGTCGCAGCGTGTGCGTCGTCGTACGTTCTGGCCGGCCCGGCCCTTGGGCGCGCGTTC 170
GTGTTGCTGCTTGTAGGCTTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGNGT 315
                         241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                    Iowa State University
035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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                                                                             301 TGGACATTGTTATGTATTAATAAATGCTTTGC 332
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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
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PCR PRimers
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BG841223.2
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/done lib="armwwoll" |
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// clone rocts were used for each of the low water potential
// clone rocts were used for each of the low water potential
// combined from each of the two time points at high water
potential (zmrwwol) Each roct was divided into 4 segments
// combined from each of the two time points at high water
potential (zmrwwol). Each roct was divided into 4 segments
// distances are from the junction of the roct apex and roct
cap): segment 1, 0-3 mm plus the roct cap; segment 2, 3-7
mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For detatils
of conditions see (1) with nutrient modifications as in
// clone lib-arity were constructed
in the lab of Hans Bohnert (University of Illinois-UC).
Total RNA was extracted by the 'hot Phenol' method (Plant
Molecular Biology manual. DS: 1-13, 2nd ed., 1997). This
method worked in eliminating carbohydrate material present
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1 (basea I to 629)

Bohnert, H., Sharp, R. B., Springer, G. K., Porcyko, V., Fredricksen, M., Sharp, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A., Topinka, C., Davis, G.B., Schachtman, D., Wu, Y. and Nguyen, H.T.

NG Grant Dal-0211842: Functional Genomics of Root Growth and Root Unpublished [2003]
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GTGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTTCTGGATGTTGTGT
                                                                                                                                                                                                                                                                                                                                                   291 GTGTTGCTTGTGTAGGCTTTGGTACGTATGGTAGGCTTTATTTGCTTCTGGATGTTGTG
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University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-2475
Eax: 217-333-5574
Email: bohnerth@life.uiuc.edu
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/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGACATTGTTATGTATAAA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 TGGACATTGTTATGTATAAA 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF625618.1 GI:37377941
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denaturing agarose gals and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from total RAWA using agarose gals and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from total RAWA using the Oligotex Direct mRNA wis isolated twice from total RAWA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a Not1 site and used to reverse transcribe the sequence tags of the root (Root-Segment). 2, 3, or 4) the sequence was tound in based on the Identification of the tag. A suffix of 80 indicates that the sequence tag, and hence the sequence identifier to designate which region of the cond in based on the Identification of the tag. A suffix of 80 indicates that the sequence tag, and hence the sequence segment, could not be identified. The double stranded cDNAs were adaptored with EcoRI adaptors at both ends, and then digested with Nor1. The CDNA was directionally cloned then digested with Nor1. The CDNA was directionally cloned the digested with Nor1. The CDNA was directionally cloned the CDNAs were adaptored with EcoRI adaptors at both ends, and the COINAS were adaptored with EcoRI adaptors at both ends, and the COINAS were adaptored with EcoRI adaptors at both ends, and the COINAS were adaptored with EcoRI adaptors at the The ADAS and the COINAS were segment of white colony forming units (cfu) in the primary libraries before amplification was as follows: mrwweb5: 3.37 x 105, zmrww90: 3 x 105. zmrw905: 3.37 x 105, zmrw90: 3 x 105. zmrw905: 3.37 x 105, zmrw90: 3 x 105. zmrw90: 3

TISSUE=Root_segment_4

ORIGIN

8 8 8 8

ACTACTIGGGTITGITGAATTATTATGANCAGTIGCGTATTGIAATTCAGCTGGGCTA-C 299

241

3529_1_42_1_H09.x_1 3529 -2 mm ear tissue from Schmidt and Hake Labs Zea mays cDNA, mRNA sequence. 240 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. 120 235 180 234 caaddrocarcecerdercaagorcegreerrraaagaceeeeeeacregeagrea 175 174 GTGTTGCTGCTTGTGTAGGCTTTGGTACGGGCTTTATTTGCTTCTGGATGTTGTT 115 /lab_host="E. coli XLOLR" /clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake /note="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoR1; Site 2: Xho1; RNA isolated by Hake lab. 1 milTion pfu amplified. Ampicillin is the selection marker." CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGTTTAAANACCCACCGGCACTGGCAGTGA GTGTTGCTGCTTGTAGGCTTTTGGTACGTATGGGCTTTTATTTTGCTTCTGGATGTTGTGT GGTCGCAGCGTGTGCGTCCGTCGTACGTTCTGGCCGGCCCGGGCCTTGGGCGCGCGATC Gaps Walbot,V. Maize EST8 from various cDNA libraries sequenced at Stanford ä 6; Length 449; Indels Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3529 1 42 1 row: H column: 09. Score 311.6; DB 6; Pred. No. 1.9e-77; 0; Mismatches 7; db_xref="taxon:4577" /tissue_type="ear" /dev_stage="2 mm" /lab_host="8. coli XLC organism="Zea mays" /mol_type="mRNA" /cultivar="B73" Query Match

Best Local Similarity 97.6%; Pre
Matches 325; Conservative 0; TGGACATTGTTATGTATT 318 CB380909.1 GI:29130205 18 recacarrerrarerar 1 (bases 1 to 449) University Unpublished (1999) 1. .449 Zea mays Zea mays EST. 301 Н 61 181 Query Match Best Local S 121 ACCESSION VERSION KEYWORDS SOURCE ORGANISM source CB380909/c LOCUS DEFINITION REFERENCE AUTHORS TITLE RESULT 15 JOURNAL FEATURES COMMENT ORIGIN g 8 유 ò 셤 ઠે 셤 ð 셤 ð 음

114 ACTACTTGGGTTTGTTGAATTATTATGAGCAGTTGCGTATTGTAATTCAGCTGGGCTACC 55

300 CTGGACATTGTTATGTATTAATAATGCTTTGC 332

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a ò Search completed: March 8, 2006, 05:42:24 Job time : 2670.19 secs

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March 8, 2006, 04:11:07; Search time 717.823 Seconds (without alignments) 3824.664 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9793542 seqs, 4134689005 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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329
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                  Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Query Match Length DB	DB		Description
-	329	100.0	332	7	US-10-603-524A-1	Sequence 1, Appli
8	329	.100.0	1236	7	US-10-425-114-13754	
1	329	100.0	7545	σ	US-10-508-166-10	
7	329	100.0	11643	σ	US-10-508-166-11	11,
2/2	327.4	99.5	1206	7	US-10-425-114-32117	3211
9	327.4	99.5	1271	7	US-10-425-114-5509	Sequence 5509, Ap
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0	301.4	91.6	1294	œ	US-10-739-930-3058	Sequence 3058, Ap
10	294	89.4	1057	7	US-10-425-114-1933	٠.
11	286	86.9	818	7	US-10-425-114-35874	٠.,
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13	278.4	84.6	1216	7	US-10-425-114-25328	Sequence 25328, A
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17	232.6	70.7	1278	7	US-10-425-114-27672	Sequence 27672, A
18	204	62.0	1057	7	US-10-425-114-2886	
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02° 0	183.2	55.7	338	æ	US-10-425-115-142679	Sequence 142679,
c 21	169.4	51.5	611	æ	US-10-425-115-108780	Sequence 108780,
22	142	43.2	1203	œ	US-10-425-115-156913	Sequence 156913,
c 23	132.4	40.2	478	œ	US-10-425-115-119522	
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Sequence 147870,	Sequence 15550, A	Seguence 23745, A	Sequence 31637, A	Sequence 167755,	Sequence 37, Appl	Sequence 171, App	Sequence 167758,	Sequence 167756,	Sequence 1977, Ap	Sequence 167753,	Sequence 108665,	Sequence 37885, A	Sequence 61981, A	Sequence 158157,	Sequence 62042, A	Sequence 7789, Ap	Sequence 299, App	300	Sequence 299, App	Sequence 300, App	Sequence 135469,
US-10-425-115-147870	US-10-767-701-15550	US-10-425-115-23745	US-10-425-114-31637	US-10-425-115-167755	US-10-310-154-37	US-10-732-923-171	US-10-425-115-167758	US-10-425-115-167756	US-10-425-115-1977	US-10-425-115-167753	US-10-425-115-108665	US-10-425-115-37885	US-10-425-115-61981	US-10-425-115-158157	US-10-425-115-62042	US-10-425-115-7789	.US-10-363-345A-299	US-10-363-345A-300	US-10-363-483A-299	US-10-363-483A-300	US-10-425-115-135469
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32.7	26.3	25.4	24.8	24.8	24.8	24.8	23.8	23.3	18.8	17.3	16.9	16.9	16.8	16.0	15.0	14.3	11.9	11.9	11.9	11.9	11.7
107.6	86.4	83.6	81.6	81.6	81.6	81.6	78.4	9.94	62	57	55.6	55.6	55.4	52.6	49.2	47	39	39	39	39	38.4
24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

	ő	09	120
PLANTS	; 0; Gaps	GCGCGCGATC 	AAGTTTGTTT AAGTTTGTTT
SEQUENCES IN TRANSGENIC 524A or G or G	Length 332; Indels	GGTCGCAGCGTGTGCTGTCGTCGTACGTTCTGGCCGGCCG	agaancgitigcgitiggcgigigigigigiticiggittigcittaathttaccaagitigitit
ENCES IN	DB 7; 1.2e-89; es 0;	2TGGCCGG	GTTTGCT
7, 524A	329; No. latch	racgrr racgrr	SCTTCTK
3524A C. C. TIO/603 25 25 2571 7 C, T, C, T, C, T, C, T, C, T, C,	Score Pred. 0, Mism		STGTGTC
1158887A1 1158887A1 1258887A1 12036887A1 1358 OF REGUL 1368 OF 25 1203-06-25 12-06-27 12-06-27 12-06-27 13-06-2	* 6	GCGTGT 	TGGCGT(
Cation U NS2004015 CON: CON: USE 50528A 110N NUMBER NATE: 2002- NN NUMBER NOS: 4	vat	606767 	rrgcgr rrgcgr
PD11 NATION 11 NATION 12 NATIO	뎔	GGTCGCAGCGTGTCCGTGTCCGTCGTACGTT	IGAANCG
LIT 1 0-603-524A-1 duence 1, Appl duence 1, Appl duence 1, Appl duence 1, Dow 1 ILLE REFERENCE; URRENT PILING RICH RILING DAY RIOR APPLICATI RICH RILING DAY RIOR RILING DAY RICH RILING DAY RICH RILING DAY RICH RILING DAY COTHER INFORMATI FEATURE; NAME/KEY: misc LOCATION: (159) OTHER INFORMATI COCATION: (159) OTHER INFORMATI COCATION: (260) OTHER INFORMATI	atch cal	н 1	61 4
RESULT 1 US-10-603-524A-1 SQUENCE 1 APPLICANT: DESCREAL INFORM PUDDICANT: DESCREAL CANT: DESCREAU FILLE REFERENC CURRENT APPLICA FILLE REFERENC CURRENT APPLICA FILLNG NUMBER OF SEG SOFTWARE: PAL SEQ ID NO 1 LENGTH: 332 TYPE: DNA COTHER INFORM FEATURE: NAME/KEY: mi LOCATION: (6 OTHER INFORM FEATURE: NAME/KEY: mi LOCATION: (6 OTHER INFORM FEATURE: NAME/KEY: mi LOCATION: (1 OTHER INFORM FEATURE: NAME/KEY: mi	Query Match Best Local Matches 33		•
8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	~~~	පි පි	& 8 8

121 CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA 180

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121
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                                                                                                                                                                                                                                        Sequence 13754, Application US/10425114
Fublication No. US20040034888A1
Fublication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Soreen, Steven B
APPLICANT: Goo, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: PlantE and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plantes and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
SEQ ID NO 13754
ILENGTH: 1236
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121 CAAGGIGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGA 180
                                                                                    241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
                                                                                                     241 ACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 329; DB 7; Best Local Similarity 99.1%; Pred. No. 2.1e-89; Matches 329; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), OTHER INFORMATION: Clone ID: LIB143-039-B10_FLI
US-10-425-114-13754
                                                                                                                                              TGGACATTGTTATTAATAAATGCTTTGC 332
                                                                                                                                                                        301 recarrerrarerararaarecrrrec 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                              301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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US-10-508-166-10 ; Sequence 10, Application US/10508166 ; Publication No. US20050223430A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3393 CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAAGACCCACCGGCACTGGCAGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GTGTTGCTGCTTGTGTAGGCTTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT
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Publication No. US2005023430A1

GENERAL INFORMATION:

APPLICANT: PLANT RESEARCH INTERNATIONAL BV

APPLICANT: BAKKER, Hendrikus A.C.

APPLICANT: BOSCH, Hendrikus B.A.

TITLE OF INVENTION: GWTIII expression in plants

FILE REFERENCE: 62862A - P033313WO

CURRENT APPLICATION NUMBER: US/10/508,166

CURRENT PILING DATE: 2004-09-17

PRIOR APPLICATION NUMBER: US-60/365,769

PRIOR FILING DATE: 2002-03-19

PRIOR FILING DATE: 2002-03-26

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATEORIL VERSION 3.2

SEQ ID NO 11

LENGTH: 11643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 329; DB 9;
Pred. No. 4.7e-89;
0; Mismatches 3;
APPLICANT: BLAKER, Hendrikus A.C.
APPLICANT: BLAKER, Hendrikus A.C.
APPLICANT: BLAKER, Hendrikus A.C.
APPLICANT: BLAKER, Hendrikus A.C.
APPLICANT: BOSCH, Hendrik J.
TITLE OF INVENTION: GNTILI expression in plants
FILE REFRENCE: 6562A - p033313WO
CURRENT APPLICATION NUMBER: US-00/365,769
FRIOR APPLICATION NUMBER: US-60/365,769
FRIOR APPLICATION NUMBER: US-60/365,769
FRIOR APPLICATION NUMBER: US-60/368,047
FRIOR FILING DATE: 2002-03-19
FRIOR FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VERSION 3.2
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Best Local Similarity 99.1%;
Matches 329; Conservative
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LENGTH: 7545
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and Other Molecules Associated With
                                                                                                                                                                            1107 ACTACTIGGGITIGITGAATTATTATGAGCAGTIGCGTATIGTAATTCAGCTGGGCTACC 1166
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                                                                GTGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGCTTTTATTTGCTTCTGGATGTTGTGT
                                                                                                1047 GTGTTGCTGCTTGTAGGCTTTGGTACGTATGGGCTTTTATTTGCTTCTGGATGTTGTGT
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APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associat
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: US/10/425,114
FILE REFERENCE: 38-21 (53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
LENGTH: 1271
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Pred. No. 6.5e-89;
0; Mismatches 4;
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US-10-425-114-5509
                                                                                                                                                                                                                                                                                                                                   US-10-425-114-5509
; Sequence. 5509, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-10-425-114-5169
; Sequence 5169, Application US/10425114
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ORGANISM: Zea mays
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Car, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)8
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                                                                                                                      Length 11643;
                                                                                                                                                          Indels
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Pred. No. 6.3e-89;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: UC-ZMFLB73264B10_FLI
US-10-425-114-32117
                                                                                                                  ; Score 329; DB 9;
Pred. No. 5.7e-89;
0; Mismatches 3;
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32117
                                                                                                                  Query Match - 100.0%;
Best Local Similarity 99.1%;
Matches 329; Conservative 0
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-508-166-11
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Best Local Similarity 98.8%;
Matches 328; Conservative
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.TYPE: DNA
ORGANISM: Zea mays
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US-10-425-114-32117
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Gaps

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Length

120

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Sequence 3058, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REPERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
SEQ ID NOS: 11088
LENGTH: 1294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.6%; Score 301.4; DB 8; 97.0%; Pred. No. 5.4e-81; iive 1; Mismatches 5;
                                                                                                       Score 315; DB 7;
Pred. No. 2.6e-85;
0; Mismatches 3
                                                 OTHER INFORMATION: Clone ID: 700443507 FLI
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                                                                                                     95.7%;
nilarity 99.1%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 97.0 Matches 326; Conservative
                                                                                                       Query Match
Best Local Similarity
Matches 315; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Zea mays
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US-10-739-930-3058
                                                         , Otton, L. SIII
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILENTER PREPRENCE: 38-21(53113)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5169
LENGTH: 725
TYPF.
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tobaska, Jack E
APPLICANT: Tobaska, Jack E
APPLICANT: Tobaska, Jack E
APPLICANT: Tobaska, Jack E
APPLICANT: APPLICANTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(3313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5111
LENGTH: 526
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Pred. No. 1.1e-85;
0; Mismatches 4
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US-10-425-114-5169
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Publication No. US20040034888A1
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Best Local Similarity 98.8
Matches 317; Conservative
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ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
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Gaps

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Length, 1294;

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CURRENT FILING DATE: 2003-04-28 UNDBER OF SEQ ID NOS: 73128 . SEQ ID NO 35874 LENGTH: 818
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ORGANISM: Zea mays
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven B
APPLICANT: Sovalic, Jack B
APPLICANT: Goo, Yongwel
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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Publication No. US20040034888A1

Fublication No. US20040034888A1

Fublication No. US20040034888A1

Fublication No. US2004003488A1

Fublicant: Liu, Jingdong

FAPLICANT: Zhou, Yihua

FAPLICANT: APPLICANT: Applicant Screen, Steven E

FAPLICANT: Cao, Yongwei

FILE REFERENCE: 38-21(53313)

FILE REFERENCE: 38-21(53313)

CURRENT APPLICATION NUMBER: US/10/425,114
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Gaps
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89.4%; Score 294; DB 7; Length 1057;
Best Local Similarity 99.0%; Pred. No. 8.8e-79;
Matches 294; Conservative 0; Mismatches 3; Indels
                                                                             1251 TACCTGGACATTGTTATGTTAATAAATGCTTTGC 1286
                                             297 TACCTGGACATTGTTATGTATAATAATGCTTTGC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: 700171786 FLI
                                                                                                                           RESULT 10
US-10-425-114-1933
; Sequence 1933, Application US/10425114
; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-425-114-35874
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 39-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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                                                                            ; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE011E01_FLI
US-10-425-114-35874
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98.6%; Pred. No. 3.4e-74;
ive 0; Mismatches 4
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US-10-425-114-5192
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; Publication No. US20040034888A1
TYPE: DNA ORGANISM: Zea mays subsp. mexicana
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Matches 279; Conservative
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TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
    APPLICANT: Liu, Jingdong
; APPLICANT: Liu, Jingdong
; APPLICANT: Soreen, Yinua
; APPLICANT: Soreen, Steven E
; APPLICANT: Soreen, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REPERENCE: 38-21 (5313) B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25328
LENGTH: 1216
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                                                               GTGTTGCTGCTTGTTAGGCTTTTGGTACGTATGGCTTTTATTTTGCTTCTGGATGTTGTT
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Best Local Similarity 98.6%; Pred. No. 5.2e-74;
Matches 279; Conservative 0; Mismatches 4; Indels 0;
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Sequence 153098, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
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US-10-425-114-36047
US-10-425-114-36047
Sequence 36047, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 153098
LENGTH: 1391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ATCAGAANCGTTGCGTTG-GCGTGTGTGCTTCTGGTTTGCTTTAATTTTACCAA-GTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGTCGCAGCGTGTGCGTCTCCGTCGTTCTGGCCGGCCGGGCC---TTGGGCGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 AGTGAGTGTTGCTGCTTGTAGGCTTTTGGTACGTATGGGCTTTATTTGCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1304 AATTCAGCTGGGCTACCTGGACATTGTTATGTATTAATAAATGCTTTGC 1352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1391;
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US-10-425-114-36047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.7%; Score 265.6; DB 8; Best Local Similarity 93.1%; Pred. No. 4.4e-70; Matches 325; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_71207C.1 US-10-425-115-153098
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(1391)
OTHER INFORMATION: unsure at all n locations
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	Gaps	racaca s7			GTTTG 4	rggcAg 1	GGCAG 4	226	STCAGG 5.	TGT 283	TGT 594
594;	15;	TTGGGG	ATTGGG	TACCA	TACCA	GGCAC	GGCAC		TCTAAG	GCGTAT	GCGTAT
Length 594;	Indels		CGGGCCTT	CTTTAATT	CTTTAATT	ANACCCAC	AGACCCCC	TTATTECT	TATTIGC	TGANCAGT	rgagcagt
71.6%; Score 235.4; DB 7; 91.9%; Pred No. 4 7e.61.	,6,5	79922957) 	TGGTTTG	GGCGTGTGTGCTTCTGGTTTGCTTTAATT	GCTTTAA	GCTTTAA	ATGGGCT	ACGGGCT	ATTATTA	ATTATTA
Score 235.4; DB 7	0; Mismatches	TACGITC	TACGTTC	TGTGCTTC	TGTGCTT	GCCCGTG	Greeren	TGGTACG	TTGTGTAGGCTTTGGTACGTACG	TTTGTTG	TTTGTTG
Score	0	TCCGTCG	TCCGTCG	GCGTGTG	GCGTGTG	GGTCAAG	GGTCAAG	PAGGCTT	raggett	ACTTGGG	ACGTGGG
71.6%;	tive	GTGCGTG	GTGCGTG	TGCGTTG	TGCGTTG	ATCGCGT	ATCGCGT	GCTTGTG	GCTTGTG	GTGTACT	GTGTACT
Query Match Best Local Similarity	Matches 274; Conservative	1 GGTCGCAGCGTGTGCGTGTCCGTCGTACGTTCTGGCCGGCC	297 GGTCGCAGCGTGTGCGTCGTCGTACGTTCTGGCCGGCCCGGGCCTTATTGGGCGCGCG 356	ATCAGAANCGTTGCCGTGTGTGTGTGCTTCTGGTTTGCTTTAATTTTACCAAGTTTG	ATCAGAAGCGTTGCGTGTGTGCTTCTGGTTTGCTTTAATTTTACCAAGTTTG	TTTCAAGGTGGATCGCGTGTCAAGGCCCGTGTGCTTTAAANACCCACCGGCACTGGCAG	TITCAAGGTGGATCGCGTGGTCCAAGGTCCGTGTAAAAGACCCCCCGGCACCGGCAG 476	TGAGTGTTGCTGCTGTGTGGCTTTGGTACGTATGGGCTTTATTTGCT		227 - TCTGGATGTTGTGTACTTGGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGT 283	537 GTCTGGATGTTGTGTACGTGGGTTTGTTGAATTATTATGAGCAGTTGCTTGTTGT
atch cal Sim	274;	.1 8:	297 GG	58 AT	357 AT	118 TT	417 TT	178 TG	477 TC	227 -T	537 GT
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Search completed: March 8, 2006, 05:20:27 Job time : 718.823 secs

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March 8, 2006, 04:19:11; Search time 885.156 Seconds (without alignments) 865.410 Million cell updates/sec
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    /cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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329
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Perfect score:
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                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 24715, A	Seguence 409218,	Sequence 815284,	Sequence 855422,	Sequence 626220,	Sequence 249647,	Sequence 249651,	Sequence 91, Appl	Sequence 917185,	Sequence 917186,	Sequence 7, Appli	Sequence 21, Appl	Sequence 53, Appl	Sequence 13269, A	Sequence 243873,	Seguence 449515,	Seguence 665533,	Sequence 750364,	Sequence 750365,	Sequence 92022, A
SUMMARIES	a ib	9 US-11-096-568A-24715	5 US-09-925-065A-409218	5 US-09-925-065A-815284	5 US-09-925-065A-855422	5 US-09-925-065A-626220	S US-09-925-065A-249647	S US-09-925-065A-249651	12 US-11-011-332A-91	S US-09-925-065A-917185	5 US-09-925-065A-917186	3 US-10-276-233A-7	12 US-11-121-086-21	9 US-11-114-798-53	3 US-10-995-561-13269	5 US-09-925-065A-243873	S US-09-925-065A-449515	5 US-09-925-065A-665533	S US-09-925-065A-750364	5 US-09-925-065A-750365	3 US-09-925-065A-92022
	Match Length DB	1676	567	582	583 (260	568	568	6499	677	677	33737 8	175100]	196716	63693	512	546	612	630	630	735 (
* Query	Match 1	55.6	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.6	10.6	10.6	10.6	10.5	10.3	10.1	10.1	10.1	10.1	10.1	10.1
	Score	183	36	35.8	35.8	35.6	35.4	35.4	35.4	34.8	34.8	34.8	34.8	34.6	33.8	33.2	33.2	33.5	33.2	33.2	33.2
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Sequence 53, Appl Sequence 51856, A Sequence 391285,	Sequence 729222, Sequence 203360, Sequence 888475,	Sequence 372789, Sequence 882494, Sequence 870022, Sequence 662035,	Sequence 662036, Sequence 662037, Sequence 328191, Sequence 866127,	Sequence 57415, A Sequence 57415, A Sequence 237472, Sequence 257298, Sequence 910742,	Sequence 1, Appli Sequence 89006, A Sequence 89007, A Sequence 46570, A Sequence 46570, A
US-11-114-798-53 US-09-925-065A-51856 US-09-925-065A-391285	US-09-925-065A-729222 US-09-925-065A-203360 US-09-925-065A-888475	US-09-925-065A-372789 US-09-925-065A-882494 US-09-925-065A-870022 US-09-925-065A-662035	US-09-925-065A-662036 US-09-925-065A-662037 US-09-925-065A-328191 US-09-925-065A-866127	US-10-750-185-57415 US-10-750-623-57415 US-09-925-065A-367472 US-09-925-065A-257298 US-09-925-065A-910742	US-09-925-065A-89006 US-09-925-065A-89006 US-09-925-065A-89007 US-09-925-065A-89008 US-09-925-065A-46570 US-10-932-182A-166756
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ALIGNMENTS

RESULT 1
US-11-096-568A-24715
; Sequence 24715, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
0,3
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
APPLICATION NU
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24715
; LENGTH: 1676
CONCANISM: Zea mays subsp. mays
FRATURE
; NAWE/KEY: misc_feature
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vative 0
Qy 140 AAGGCCCGTGTGTTTAANACCCACCGGCACTGGCAGTGAGTGTTGCTGCTTGTGTGTAGG 199
Db 1476 AAGCCGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Qy 200 CTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGTACTACTTGGGTTTGTAA 259
Db 1536 CTTTGGTACGTATGGCTTTATTTGCTTCTGGATGTTGTGTACTACTTGGGGTTTGTGA 1595
Oy 260 TTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACCTGGACATTGTTATGTATTA 319
Db 1596 TTATTATGAGCAGTTGCGTATTGTAATTCAGCTGGGCTACCTGGACATTGTTATGTATTA 1655
Qy 320 ATABANGCTTYGC 332
Db 1656 ATAAATGCTTTGC 1668

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SEQ ID NO 855422
LENGTH: 583
SEQ ID NO 815284
                             LENGTH: 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 TATGGTAATAGATTTTAAAAGATGTTTTAAAAGGAGCTCAATGGTTAAAAGTCAGCTTAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 TTAAANACCCACCGGCACTGGCAGTGAGTGTTGCTGCTTGTGTAGGCTTTGGTACGTATG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 GCCTTTATTTGCTTCTGGATGTTGTGTACTACTTGGCTTTGTTGAATTATTATGANCAGT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GCCTTCATGTTGTTGTTTTTTTTCTTCTCTAGGACCTTGTCTCTTTTTTGAGGAAA 60
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GENERAL INFORTALION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-6

PRIOR PILING DATE: 2000-11-6

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
                                                                                                                               APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Mucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION MURBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASISEQ for Windows Version 4.0
SEROIT DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%; Score 36; 48.0%; Pred. No.
                                                 Sequence 409218, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 815284, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 TGCGTATTGTAATTCAGCTG 293
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Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type: DNA GARANISM: Homo sapiens US-09-925-065A-409218
                          US-09-925-065A-409218/C
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                                                                                                                                                                                                                                                                                                                                                                         245 TCCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTTTTTATAAAAGGCTTTCATG 304
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                                                                                                                                                                                                                                                                                                                                                                                                                             225 CTTCTGGATGTTGTGTACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATT 281
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                                                                                                                                                                                                                                                                                                                  165 CCGGCACTGGCAGTGATGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTACCAAGTTTGTTTCAAGGTGGATCGCGTGGTCAAGGCCCGGTGTGCTTTAAANACCCA
                                                                                                                                                                                                                105 TITACCAAGTITGTITCAAGGTGGATCGCGTGGTCAAGGCCCGTGTGCTTTAAANACCCA
                                                                                                                                                              Gaps
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: NUCleotide Polymorphisms in the Human Genome
FILE REFERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PRILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-30
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                                                                                                     Score 35.8; DB 6; Length 5:
Pred. No. 1.7;
0; Mismatches 89; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 855422, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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US-09-925-065A-626220
; Sequence 626220, Application US/09925065A
; Publication No. US20040181048A1
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                                                                                                        10.9%;
                                                                                             Query Match
Best Local Similarity 49.7%
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-815284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-925-065A-855422
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                     TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT PELING DATE: 2009-10-80-8
FRIOR APPLICATION NUMBER: US 60/243,096
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-11-20
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-10-46
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PRESERE OF Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 45; Indels
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10.8%; Score 35.4; DB 6;
Best Local Similarity 57.3%; Pred. No. 2.3;
Matches 63; Conservative 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
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PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 249647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 249647, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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57.9%;
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Best Local Similarity 57.94
Matches 62; Conservative
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GENERAL INFORMATION:
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LENGTH: 560
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209 GTATGGGCTTTATTTGCTTCTGGATGTTGTGTACTACTTGGGTTTGTTGAATTATTATGA

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FOR PREDICTION OF TREATMENT RESPONSE AND/OR SU
209 GTATGGGCTTTATTTGCTTCTGGATGTTGTGTACTACTTGGGTTTGTTGAATTATTATGA
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                                                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                269 NCAGTIGCGIATIGIAATICAGCIGGCTACCIGGACATIGITATGTATT 318
                                                                                              443 GCATGTGCTTACTTTATGACATAAGATGTTTCAGGCTAATTTTGTGTATT 492
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-36
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR PILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                    Sequence 249651, Application US/09925065A Publication No. US20040181048A1
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APPLICANT: Adorjan, Peter
TITLE OF INVENTION: PROGNOSTIC MARKERS
TITLE OF INVENTION: BREAST CELL PROLIF
FILE REFERENCE: 47675-99
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Publication No. US20060024684A1
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Mueller, Volkmar
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Nimmrich, Inko
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APPLICANT: Harbeck, Nadia
APPLICANT: Koenig, Thomas
APPLICANT: Maier, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martens, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rujan, Tamas
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CORGANISM: Homo sapiens
US-09-925-065A-249651
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Best Local Similarity
Matches 63; Conserval
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 917185
LENGTH: 677
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Publication No. US20040181048A1
GENERAL INFORMATION:
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Best Local Similarity 60.0
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                57; Conservative
                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-917185
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US-09-925-065A-917186
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Matches 57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3664 TATGAGGTAAAGGTAAAGATTTAATTGATATAGGTTATGATAGAGGTGTTGATTTTGTG 3723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 CGTATGGGCTTTTATTTGCTTCTGGATGTTGTACTACTTGGGTTTGTTGAATTATTATG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 TTCTGGTTTGCTTTAATTTTACCAAGTTTGTTTCAAGGTGGATCGCGTGGTCAAGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 TGTGCTTTAAANACCCACCGGCACTGGCAGTGAGTGTTGCTGCTTGTGTAGGCTTTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 917185, Application US/09925065A; Publication No. US2040181048A1; Publication No. US2040181048A1; GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome; FILE REFERENCE: 108827.135; CURRENT APPLICATION NUMBER: US/09/925,065A; CURRENT APPLICATION NUMBER: US 60/25,065A; CURRENT PILING DATE: 2001-08-08; PRIOR PILING DATE: 2000-10-24; PRIOR PILING DATE: 2000-11-20; PRIOR APPLICATION NUMBER: US 60/252,147; PRIOR PILING DATE: 2000-11-30; PRIOR APPLICATION NUMBER: US 60/250,092; PRIOR APPLICATION NUMBER: US 60/261,766; PRIOR APPLICATION NUMBER: US 60/261,766; PRIOR APPLICATION NUMBER: US 60/261,766; PRIOR PILING DATE: 2001-01-16; PRIOR APPLICATION NUMBER: US 60/261,766; PRIOR APPLICATION NUMBER: US 60/269.846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 ANCAGITGCGIAITGIAAITCAGCIGGCIACCIGGACAITGIIAIGIAIT 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-11-011-332A-91
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                                        CUKREW FILLING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: US 10/517,741
PRIOR PELING DATE: 2003-10-01
PRIOR PELING DATE: 2003-10-01
PRIOR PELING DATE: 2003-10-01
PRIOR PILING DATE: 2003-10-01
PRIOR PILING DATE: 2003-10-01
PRIOR PELING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR PILING DATE: 2003-04-17
PRIOR PILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 0317955.0
PRIOR PILING DATE: 2004-12-13
PRIOR PELING DATE: 2003-04-17
PRIOR PELING DATE: 2003-04-17
PRIOR PILING DATE: 2004-12-13
PRIOR FILING DATE: 2004-12-11
PRIOR PILING DATE: 2004-03-10
PRIOR PILING DATE: 2004-03-30
PRIOR PILING DATE: 2004-03-30
PRIOR PILING DATE: 2004-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%; Score 35.4; Di 46.8%; Pred. No. 4.6;
CURRENT APPLICATION NUMBER: US/11/011,332A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 108; Conserv
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US-09-925-065A-917185
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LENGTH: 6499
                           CURRENT
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                                                                                            Gaps
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE PREPERENCE: 108877.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-01-16
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Pred. No. 3.5;
0; Mismatches 38; Indels (
10.6%; Score 34.8; DB 6; Length 677; 60.0%; Pred. No. 3.5; ive 0; Mismatches 38; Indels
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Publication No. US20050260572A1
ENDICATION NO. US20050260572A1
APPLICANT: DNA Chip Reasearch Inc.
APPLICANT: Hitachi Software Engineering Co., Ltd.
TITLE OF INVENTION: A method of predicting cancer condition
FILE REFERENCE: PH-1533-PCT
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PAPLICANT: MARQUEZ, ABBEY
TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: POULSEN, KIRSTEN V.
TITLE OP INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138 6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
PRIOR APPLICATION NUMBER: 2005-05-04
PRIOR APPLICATION NUMBER: 2005-05-04
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Pred. No. 11;
0; Mismatches
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   PRIOR APPLICATION NUMBER: US/10/276,233A
PRIOR PLICATION NUMBER: JP 2001-73063
PRIOR PILING DATE: 2001-03-14
PRIOR PLING DATE: 2001-04-06
PRIOR PLING DATE: 2001-08-02
SOFTWARE: PACENTIN VET: 3.2
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CURRENT APPLICATION NUMBER: US/10/276,233A
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Publication No. US20050266459A1
GENERAL INFORMATION:
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Publication No. US20060035246A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
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Best Local Similarity 60.0%;
Matches 57; Conservative
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60.0%;
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Best Local Similarity 60.0
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-11-121-086-21
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LENGTH: 175100
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31777 Catadataggtgttagáttttgtcadatgcitttttttgcatcadthatatatatgtatg 31836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13269, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (FILE REFERENCE: CL001559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48774 CATAATTTCATTATTCACCCAAAAGTCATTCAGGAGCATGTTGTTTGATTTCCATGTAAT
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Pred. No. 26;
0; Mismatches 124;
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Pred. No. 22;
0; Mismatches
CURRENT APPLICATION NUMBER: US/11/114,798
CURRENT FILING DATE: 2005-04-26
FRIOR APPLICATION NUMBER: 10/173,525
FRIOR FILING DATE: 2002-06-17
FRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver: 3.3
SEQ ID NO 53
LENGTH: 196716
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 13269
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                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 57.5%;
Matches 61; Conservative
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; ORGANISM: Homo sapiens
US-10-995-561-13269
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Best Local Similarity
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RESULT 15
US-09-228-065A-243873
i Sequence 243873
i Sequence 243873
i Sequence 243873
i Sequence 243873, Application US/09925065A
i Publication No. US20040181048A1
i Sequence 243873 David G.
i TITLE OF INVENTION: Identification and Mapping of Single
i TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
i TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
i TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
i TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
i TITLE OF INTORATION NUMBER: US 60/243,096
i PRIOR PILING DATE: 2000-10-24
i PRIOR PILING DATE: 2000-11-20
i PRIOR PILING DATE: 2000-11-16
i PRIOR PILING DATE: 2000-11-16
i PRIOR PILING DATE: 2001-01-16
i PRIOR PILING DATE: 2001-01-16
i PRIOR PILING DATE: 2001-05-09
i NUMBER: US EQ ID NOS: 957086
i SOFTWARE: Fast-SEQ for Windows Version 4.0
i SEQ ID NO 243873
i LANGTH: 512
i TYPE: DNA
i ORGANISM: Homo sapiens
US-09-925-065A-243873
i Guery Match
Best Local Similarity 58.9%; Pred, No. 9.2;
i Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps
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Search completed: March 8, 2006, 06:10:10 Job time: 887.156 secs

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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1333 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Appli
Sequence 6335, Ap
Sequence 1476, A
Sequence 2, Appli
Sequence 16137, A
Sequence 16137, A
Sequence 16136, A
Sequence 17305, A
Sequence 17305, A
Sequence 17305, A
Sequence 1888, A
Sequence 1888, A
Sequence 1888, A
Sequence 1888, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Appli
Sequence 16819, A
                                                                                7, 2006, 23:00:44; Search time 139.621 Seconds (without alignments) 4226.797 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14882, A
Sequence 14883, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14881,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                            1 ggtcgcagcgtgtgcgtgtc......tgtattaataaatgctttgc 332
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                  2606114
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/cgn2 6/ptodata/1/ina/5_COMB.seq:*
/cgn2 6/ptodata/1/ina/6A_COMB.seq:*
/cgn2 6/ptodata/1/ina/6B_COMB.seq:*
/cgn2 6/ptodata/1/ina/H_COMB.seq:*
/cgn2 6/ptodata/1/ina/P_CTUS COMB.seq:*
/cgn2 6/ptodata/1/ina/PP_COMB.seq:*
/cgn2 6/ptodata/1/ina/PP_COMB.seq:*
/cgn2 6/ptodata/1/ina/PP_COMB.seq:*
/cgn2 6/ptodata/1/ina/PP_COMB.seq:*
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US-09-949-016-16136
US-09-949-016-12896
US-09-248-796A-1471
US-09-949-016-15854
US-09-949-016-15854
US-09-949-016-11868
US-09-949-016-117119
US-09-103-840A-2
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US-09-949-016-16774
US-09-409-800B-2
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-09-313-294A-6335
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US-09-949-016-14886
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-09-949-016-14884
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                                                                                                                                                                                                                                                   1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-851-896-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - nucleic search, using sw model
                                                                                                                                                                                                        IDENTITY_NUC Gapop 10.0 , Gapop 10.0
                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                            US-10-603-524A-1
329
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Match Length DB
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                                                                                    March
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44/8222109876
                                                                                    Run on:
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                                                                                                                                               Title:
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2582, Ap
221, App
221, App
16332, A
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Sequence 10, App
Sequence 2582, 1
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,630
FILING DATE: 10-AUG-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,590
FILING DATE: 25-AUG-1993
PRIOR APPLICATION NUMBER: US 07/669,433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/669,433
PRICHAG DATE: 15-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9006017.9
FILING DATE: 16-MAR-1990
ATTOMNEY/AGENT INFORMATION:
NAME: XOKULIS, PAUL N
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 215964/SEE35669USCIP
TELECPHONE: (202) 861-3000
US-09-949-016-14888
US-09-949-016-11747
US-09-949-016-11747
US-09-949-016-12835
US-09-949-016-12835
US-09-949-016-12835
US-09-949-016-15285
US-09-949-016-15698
US-09-949-016-15698
US-09-949-016-15698
US-09-949-016-15698
US-09-513-999C-2582
US-09-513-999C-2582
US-09-949-016-16333
US-09-949-016-11874
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ELY, SUSAN
APPLICANT: EVANS, IAN J
APPLICANT: SCHUCH, WOLFGANG W
TITLE OF INVENTION: ROOT-SPECIFIC PROMOTER
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: CUSHWAN DARBY & CUSHWAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08288630
Patent No. 5837848
GENERAL INFORMATION:
                         148405
148405
148405
148405
148405
26134
145812
767677
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10758
10758
26867
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285986
288031
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: POLYNCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR PILE REFERENCE: PL-0017 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 Gecegescringgegarc-agaageragerageringscargingscrincgrinerigeri 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 TGCTTTAATTTTACCAAGTTTGTTTCAAGGTGCATCGCGTGGTCAAGGCCCGTGTGCTTT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 ercerescernescescesarradaase-raserascerrescarerererreserraserres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 ATTAAGGTGGATCGCGTGACTCTGGCAGTGAGTGTTGCTGCTTGTGTAGGACGTGGTACG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 GTTTGCTTTTACCAAAAGTTTGTTTCAAGGTGGATCGCCTGGTCAAGGTCGTGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                              38 GGCCGGGCCTTGGGCGCGCGATCAGAANCGTTGCGTTGGCGTGTGTGTGTTCTGGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 AAANAC-----CCACCGGCACTGGCAGTGAGTGTTGCTGCTTGTGTAGGCTTTGGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TGTTGTGTACTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 CITITAATITITACC--AAGITITGTITCAAGGIGGAICGCGIGGICAAGGCCCGIGIGCITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 GCCCGGCCCTTGGGCGCGCGATCAGAANCGTTGCGTTGGCGTGTGTGT--GCTTCTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTTTGTTGA---ATTATGAGCAGCTGCGTGTTGTAATTCGGCTGGGCTACCTGGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 GGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACCTGGA 304
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                                                                                                                                                                                                                                                                                                             Length' 758;
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                                                                                                                                                                                                                                                                                                                                                               61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700351622H1
                                                                                                                                                                                                                                                                                                                Ouery Match 25.8%; Score 84.8; DB 2; Best Local Similarity 68.2%; Pred. No. 4.4e-18; Matches 202; Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76.6; DB 3;
Pred. No. 1.5e-15;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/313,294A CURRENT APPLICATION NUMBER: 1999-05-14 NUMBER OF SEQ ID NOS: 7600 SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 17
COTHER INFORMATION: a, t, c, g, or other US-09-313-294A-6335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6335, Application US/09313294A Patent No. 6476212 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 TATGGGCTTTATTTGCTTCTGGA--
                      TELEFAX: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.3%;
76.4%;
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Best Local Similarity 76.4
Matches 146; Conservative
                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
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LENGTH: 291
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US-08-288-630-2
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                                                                                                                                                                                                                                                                                                                  82 GTGTGCTTCTGGTTTGCTTTTAATTTTACC--AAGTTTGTTTCAAGGTGGATCGCGTGGTC 139
                                                                                                                                                                                                                                                                                                                                                                                                              140 AAGGCCCGTGTGTTTA----AANACCCACCGGCACTGGCAGTGAGTGTTGCTGCTTG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTGGA-------232
                                                                                                                                                                                                                    TGTTGTGTACTACTTGGGTTTGTTGAATTATTATGANCAGTTGCGTATTGTAATTCAGCT
                                                                                                                                                                        Gaps
                                                                                                                                                                     32;
                                                                                                                    Score 91; DB 2; Length 1333;
Pred. No. 5.1e-20;
                                                                                                            27.7%; Score >+, 64.7%; Pred. No. 5.1e-20; +ive 0; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.

ZIP: 2005-3918

COMPUTER READBLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,630
FILLING DATE: 10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,590
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/669,433
FILING DATE: 15-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9006017.9
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL NUMBER: 16,773
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 215964/SEE35669USCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ELY, SUSAN
APPLICANT: EVANS, IAN JAN APPLICANT: SCHUCH, WON TAPPLICANT: SCHUCH, WONTGANG W
TITLE OF INVENTION: ROOT-SPECIFIC PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1292 GGCTACCTGGATGCGGTTAATAATT 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCTACCTGGACATTGTTATGTATT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 New York Avenue, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08288630 Patent No. 5837848 GENERAL INFORMATION:
                                                                                                                                                                     Matches 211; Conservative
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-288-630-2/c
                                                           ; MCLECOLE 1
US-08-288-630-1
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                                                                                                                         Query Match
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209

155 322

97

Gaps

248

Gaps

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GENERAL INFORMATION:
                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16774
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                                                                                                                                                                                                                                                                TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28153 GAAAAGCGTACTTCTCAATCTTACCTGCTCACTGAACTGGGTATGGGAGAAATAAGAGAA 28094
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%; Score 37.6; DB 3; Length 67643;
53.0%; Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FEBSICE for Windows Version 4.0
SEQ ID NO 14760
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CURRENT FILING DATE: 2000-04-14
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Sequence 14760, Application US/09949016
Patent No. 6812339
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Patent No. 6812339
                                                      156 AAANACCCACCGGC---ACTGGCAGTG
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PRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CCATION: (1)...(67643); OTHER INFORMATION: n = A,T,C or GUS-09-949-016-14760
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Matches 79; Conservative
                                                                                                                                                                 245 GGGTTTTATTT 255
                                                                                                                                213 GGGCTTTATT 223
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51364 GGGTGGTCATGCCTTTGGCGTACAGGGACAAAATCTGGCTGTCCATCTGTGTGATACGCG 51305
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                                                                                                                                                                                                                                                            Length 17146;
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Pred. No. 0.87;
0; Mismatches 67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Straiey, Susan C.
APPLICANT: Fetherston, Jacqueline D.
APPLICANT: Lindler, Luther E.
APPLICANT: Plano, Gregory V.
TITLE OF INVENTION: Plasmid DNA From Yersinia Pestis
FILE REFERENCE: 960296.95339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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Pred. No. 3.7;
0; Mismatches
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRACESEQ for Windows Version 4.0
SEQ ID NO 16774
LENGTH: 17146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51244 GCTCGATTTĊGĊĊĠTĊGTCĠCATAGCAĠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blattner, Frederick R.
APPLICANT: Burland, Valerie
APPLICANT: Rose, Debra J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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Best Local Similarity 51.3%;
Matches 78; Conservative
                                                                                                                                                                                                                                                              10.8%;
52.8%;
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Perna, Nicole
Perry, Robert D.
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.8
Matches 75; Conservative
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RESULT 7 US-09-949-016-16137

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Sequence 17305, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
                                                                                                                              PEQUENCE LING BALGAS APPLICATION OF USING STATES ASSOCIATED APPLICANT VENTER. J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRANKE: FRAN
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Pred. No. 13;
0; Mismatches
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Pred. No. 13;
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                        Application US/09949016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
Matches 60; Conserv
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; ORGANISM: Human
US-09-949-016-17305
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LENGTH: 451924
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                     PAGENT NO. 681239
GENERAL INFORMATION:
PAGENT VENTER, OF CRAIG et al.
APPLICANT: VENTER, OF CRAIG et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILLE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER: 06/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: 66/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: PABLES OF MINGOWS VETSION 4.0
SEQ ID NO 16137
LENGTH: 126176
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERBENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/49,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR PLIING DATE: 2000-10-03
PRIOR PLIING DATE: 2000-10-03
PRIOR PLIING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRACESEQ for Windows Version 4.0
SEQ ID NO 16:38
LIENGTH: 126176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121156 GGIGTATTATGTTTTTGATGTGCTGTTGGATTCGGATTGGTATTTTGTTGAAAAATT 121215
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Pred. No. 6.6;
0; Mismatches
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Sequence 16137, Application US/09949016
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Sequence 16138, Application US/09949016
Patent No. 6812339
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ilarity 57.7%;
Conservative (
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Best Local Similarity 57.7%;
Matches 60; Conservative
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Best Local Similarity
Matches 60; Conserv
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US-09-949-016-16137
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US-09-949-016-16138
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-03

PRIOR FILING DATE: 2000-0-09-08

NUMBER: OF SEQ ID NOS: 207012

SOFTWARE: FRACES FREED for Windows Version 4.0
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                                                                                                                                        14748 CATAATÍTCATTÁTTCÁCCCÁAAAGTCATÍTCAGGAGCATGÍTÍGTÍTGATÍTÍCCÁTGTAAT 44807
                                                                                                                                                                                                                                                                                                                                                    44868 AGTGTTTGGTATGATTTTGGTTCTTTGGCACTTGCTGAAGATTGTTTATGTCCAATT 44927
                                                                                                                                                                                           204 GGIACGIATGGCTTTATTTGCTTCTGGATGTTGTGTACTTGGGTTTGTTGAATTAT 263
                                                                                       144 CCCGTGTGCTTTAAANACCCACCGGCACTGGCAGTGAGTGTTGCTGCTTGTGTAGGCTTT 203
                                                                                                                                                                                                                                                                                                264 TATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACCTGGACATTGTTATGATAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 TGGCAGTGAGTGTTGCTGCTTGTGTAGGCTTTTGGTACGTATGGGCTTTATTTTGCTTCTGG 231
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.1%; Score 33.2; D
51.0%; Pred. No. 23;
ive 0; Mismatches
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Patent No. 6812339
GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
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US-09-949-016-17119/c
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ORGANISM: Human
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APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US /09/248,796A

CURRENT PILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR PILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13
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Patent No. 6812339

GENERAL INFORMATION:
Patent No. 681234

GENERAL INFORMATION:
TITLE OF INVERTION:
TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVERTION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 15854

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 ATTTGCTGCTGGATTGAGGATGCTATAGTATTACCAGCAGCAGAATACAAAGGTTGAGAT 423
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340306 TTGTGTTTACATTCAGGGATATTGGCCTATAGTTTTCTATT 340349
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Pred. No. 0.6;
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Pred. No. 5.7;
0; Mismatches 124; Indels
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Patent No. 6747137
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Best Local Similarity 52.1%;
Matches 74; Conservative
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Begt Local Similarity 48.6%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Candida albicans
US-09-248-796A-1471
                                                                                                                                     US-09-248-796A-1471/C
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; ORGANISM: Human
US-09-949-016-15854
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US-09-949-016-15854
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: PLESCHAMA:
APPLICANT: FLESCHAMA:
APPLICANT: FLESCHAMA:
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFRENCE: 24566-20007.00
CURRENT APPLICATION NUMBER: U5/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTING DATE: 1998-06-24
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.1%; Score 33.2; DB 3; Length 4403765; Best Local Similarity 51.0%; Pred. No. 88; Matches 77; Conservative 0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.2; DB 3; Length 308362; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                   FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
FRIOR PILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 17119
LENGTH: 308362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4403765
TYPE: DNA
ONGANISM: Mycobacterium tuberculosis
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

NAME/KEY: misc_feature

LOCATION: [1]...(308362)

OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.0%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
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Search completed: March 7, 2006, 23:09:16 Job time : 154.621 secs

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/db_xref="taxon:4577"
/tissue type="Vegetative Shoot Apical Meristem (SAM) and leaf prinordia staged pl.P4"
/lissue type="Wegetative Shoot Apical Meristem (SAM) and leaf prinordia staged pl.P4"
/lab host="XII-Blue"
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/lab host="XII-Blue"
/note="forgan: Shoot apex; Vector: Uni-Zap XR; Site 1:
ECORI; Site 2: Xhoi; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged Pl-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25.
ds-CDNA molecules were generated as follows. First-strand CDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 692)
Chen, H.D., Zhang, X., Zhou, R.L., Arias L, A.C., Shendelman, J.M.,
Zazubovits, N., Borsuk, L.A., Emrich, S.J., Ashlock, D.A., Scanlon, M.J.
and Schnable, P.S.
Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D04.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B KJ. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-6256
Fax: 515-294-6256
Email: schnabl@distate.edu.
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BM381133
BM380521
BM380520
BM380520
BM3822943
AI 622731
CCA402202
CCA4022121
CCA4022121
CCA4022121
CCA402211
BM074032
CCA502933
BM074032
CCA50293
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273
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Zea mays
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                                            260.2
258.8
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DN204218/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
COMMENT
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CF626836 zmrw805_0
CF627673 zmrw805_0
BE639295 946020802
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BE186822 946012404
BE186822 946012404
BM888756 952068402
AW191435 687028F09
BU079762 946147C04
BM48022 952032D09
DR906452 E0808 Zea
BI180447 949036H01
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687009G02
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952032D09
660053H10
                                                                                                                                              8, 2006, 04:07:00 ; Search time 2337.81 Seconds (without alignments) 5823.847 Million cell updates/sec
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                                                                                                                                                                                                                                                                                        1 agccggctttatgtgcgtag.....tgtgagtggtcctatatcaa 291
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AI738207
AW061962
BQ163609
BQ163007
AW519844
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                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                   41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         - nucleic search, using sw model
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CF061154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
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291
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Query
Match Length DB
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9b est2: *
9b est2: *
9b est4: *
9b est4: *
9b est6: *
9b est7: *
9b gs82: *
9b gs82: *
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96.2
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of

Total number Minimum DB Maximum DB

Database

Searched:

score:

Title: Perfect

Sequence:

OM nucleic

Run on:

Scoring table:

BM498022 DR906452 BI180447

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285.8 285.8 282.6 281.6 281.6 281.6 2019.8 2

Result

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EST 28-FEB-2005

AI622731 486106A12 CA402201 ELO1N0433 DN221272 MEST1111 CD434915 ELO1N0330 DN223155 MEST1138 DN223155 MEST1138 CD445358 ELO1N0450 BU572221 5198403.9 CD445358 ELO1N0450 BM074032 MEST79-CO CO529353 3530 1 19 BM380681 MEST523-D BM865245 952068E09

MEST543-B 486027B11 MEST1014

486086F12 MEST14-F0 MEST14-F0

BG840667 BM381193 FEATURES

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The resulting DNA: NAW hybrid was treated with RNase H and used as a template for DNA Poll-catalyzed second strand used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of Econl adaptors, the establishment of Econl adaptors, the establishment of Econlary adaptors, the establishment of Econlary specked to be 5600 bp. The resulting molecules were directionally cloned into the Econland Khol sites of the Uni-Zap KR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XLI-Blue cells and ExAssist helper phage. Excised phagemids were titered in Solk cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: ("minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. Coli, vector, and organalle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the clones in this library lack an Xhol site at their 3, ends."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AATTTGGGGGGCTCCCCGGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 692;
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98.9%; Score 287.8; DB 8;
Best Local Similarity 99.3%; Pred. No. 3.4e-77;
Matches 289; Conservative 0; Mismatches 2;
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Best Local Similarity
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EST 02-OCT-2003
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                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
                      s 451 bp mRNA linear EST 02-OCT-20
_0B20-003-903.82 zmrws05 Zea mays cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 217-333-5574
Email: bohnerth@life.uiuc.edu
                                                                                           GI:37380107
                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Hans Bohnert
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                                                                                        CF626836.1
                                            Zmrws05_C
CF626836
                                                                                                                                            Zea mays
Zea mays
CF626836/c
                                            DEFINITION
                                                                                                                                                                   ORGANISM
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                       AUTHORS
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Coration/Onalifiers

1. 43

// Organism-sza mays:
// Ob_xtes-racon.427;
// Ob_xtes-racon
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ORIGIN

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/organism="Zea mays"
/mol type="mkNA"
/mol type="mkNA"
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/clone lib="armrws05"
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/clone lib="armrws05"
/clone lib="armrws05"
/note="Samples were collected in Robert E. Sharp's lab
(University of Missouri-Columbia) to construct three
(University of Missouri-Columbia) to construct three
normalized cDNA libraries. Dark-grown maize seedlings with
primary roots 12-20 mm in length were transplanted to high
(-0.03 MPa) or low water potential (-1.6 MPa) vermiculite,
and harvested at 5 h and 48 h after transplanting. About
1,000 roots were used for each of the low water potential
libraries (armrws05 and armws48) while 500 roots were
combined from each of the two time points at high water
potential (zmrww00). Each root was divided into 4 segments
ethylene production. Plant Physiology (Rockville). 122(3). March, 2000. 967-976. TAG TISSUB-ROot_segment_2 TAG_EEQ-ACCGA"
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Bohnart, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredricksen, M., Sharp, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A., Topinka, C., Davis, G.E., Schachtman, D., Wu, Y. and Nguyen, H.T. NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root Signaling Under Drought
                                                                                                                                                                                                                                                                                                                                                  230
                                                                                                                                                                                                                                                                                                                                                                                                       61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                        169 AATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTT 110
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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Zmrwg05 0B20-014-a07.83 zmrwg05 Zea mays cDNA 3', mRNA sequence.
CF627673.1 GI:37381557
EST.
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                                                                                                                                                                               Length 451;
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                                                                                                                                                                                                                                    Indels
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University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
121: 217-265-5475
Fax: 217-333-5574
                                                                                                                                                                      Score 285.8; DB 6;
Pred. No. 1.3e-76;
0; Mismatches 2;
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                                                                                                                                                                   98.2%;
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Matches 287; Conservative
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CF627673/c
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REFERENCE AUTHORS

TITLE

FEATURES

KEYWORDS

was converted to double-stranded characteries by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different esgment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a Nor1 site and used to reverse transcribe the segment-specific maNABs into cDAAs. Each library contains all four tags. A suffix (si. 52, s3, or 4) the sequence was found in based on the identifiest to designate which region of the root (Root_segment_1, 2, or 4) the sequence was found in based on the identifiest to designate which region of the root (Root_segment_1, 2, or 4) the sequence was found in based on the identifiest of the tag. A suffix of s0 indicates that the sequence tag, and hence the stranded cDNAs were slaze-selected (1450 bp). Size selected cDNAs were adaptored with EcoRI adaptors at both ends, and then digested with Not1. The cDNAs was directionally cloned into EcoRI-Not1 digested pBS II SK(+) phagemid vector (Stratagaene) and electroporated into E.coll in the total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw905: 3.37 x 106; zmrw408: 4.87 x 106; zmrw900: 3 x 106. The background of empty clones was less than 1%. Inserts ranged from -0.5kb to >2.5 kb, as determined by RPCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a fellows; representing the entire CDNA population cloned in each library, were used as a driver for normalization. Hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was zarried out for 4 hours as 130c.

Non-hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones was less than 1%. Insert was zarried out for 4 hours as 130c.

Insert size, determined by RPC of the entire library, ranged from 0.5kb to 2.5kb (1) Sharp R B; Silk W K; Haiao T C Growth of the Maize Primary Root elongation at low water potentials By restricting ethylen (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 4, 12-20 mm. (For detarils of conditions see [1] with nutrient modifications as in of conditions see [1] with nutrient modifications as in of the lab of Hans Bohnert (University of Illinois-UC). Total RNA was extracted by the 'hot Phenol' method (Plant Molecular Biology manual. D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)+mRNA was sconverted to double-stranded cDNA and tagged by using 289 AGCCGGCTTTATGTGCCTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACTAT 230 61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA 120 229 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTTATGACTGTCGTCAGTAA 170 9 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT Gaps ö 6; Length 675; Score 285.8; DB 6; Length 6 Pred. No. 1.4e-76; 0; Mismatches 2; Indels TAG_TISSUE=Root_segment_3 98.2**%**; 99.3**%**; Query Match
Best Local Similarity 99.33
Matches 287; Conservative

ORIGIN

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us-10-603-524a-2.rst

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CF061011 CT Zea mays cDNA clone QCT16d11, yg QCT Zea mays cDNA clone QCT16d11, yg QCT Zea mays cDNA clone QCT16d11, mRNA sequence.
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201 AATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTT 142
                                       240
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93, the Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTCTTTGCTGCTGTCGAATGACACTAT
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                                         GIGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGGAAGCCCTTTAAACTGTTGTCA
                                                                            141 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTTGGGAAGCCCTTTAAACTGTTGTCA
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/mol_type="mRNA"
/cultivar="f333 or f334"
/db_xref="taxon:4577"
/clone="QCT16d11"
/tissue_type="seedling minus kernel"
/clone_lib="QCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 282.6; DB 6;
Pred. No. 1.2e-75;
0; Mismatches 4;
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98.6%;
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CF061154/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between Imm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
                                                                                                                                                                                                                                                                                                                   448 bp mRNA linear BST 30-AUG-2000 946 - tassel primordium prepared by Schmidt lab Zea
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:4577"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
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Maize EST8 from various cDNA libraries sequenced at Stanford
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
855 Fax: 650 723 2227
Fax: 650 728 8221
Email: walbockestanford.edu
Plate: 946020 row: E column: 02.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.8%; Score 284.6; DB 2;
llarity 98.6%; Pred. No. 3e-76;
Conservative 0; Mismatches 4;
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/mol_type="mRNA"
/cultivar="OH43"
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mays cDNA, mRNA sequence.
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BE639295.1 GI:9952607
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Unpublished (1999)
Contact: Walbot V
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Walbot,V.
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                                                                                                                                                                                                                                          93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                            Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
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98.3%; Pred. No. 3.8e-75;
ive 0; Mismatches 5; Indels
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/tissue type="seedling minus kernel"
/clone lib="QCT"
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/mol type="mRNA"
/cultivar="f333 or f334"
/db_xref="taxon:4577"
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Interary was prepared by George Rudenko using poly (A) espected RNA and Universal Riboclone CDNA Synthesis System (Promesa). CDNA was synthesized using both random and oligo (dT) primers in separate reactions and equipped with EcoRl adaptors. Library was size-fractionated on agarces gels (for insert size >400bp) and non-directionally cloned into EcoRl-digested pully vector. Blue/white selection on carbenicillin-containing plates was used to recover
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Maize ESTs from various cDNA libraries sequenced at Stanford
University
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/cultivar="BMS (Black Mexican Sweet)"
/cultivar="BMS (Black Mexican Sweet)"
/tissue type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
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                                                        Unpublished (1999)
Conteact: Walbot V
Conteact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, US/
Tal: 650 723 2227
Fax: 650 728 8221
Email: walbotderanford.edu
Plate: 952067 row: E column: 09.
Location/Qualifiers
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Zea mays
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIGGCGGGGGCCCTGGAGCCCGGTCTGGGTTGGGAAGCCCTTTAAACTGTTGTCA 240
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                                              Maize ESTs from various cDNA libraries sequenced at Stanford University
University
Unpublished (1999)
Contract: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952066 row: H column: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 AGCCGGCTTTATGTGCCTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 AATTIGGGGGCTCCCCGTAIGAGAIGCIGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTT
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| Corganisma="Zea mays" |
| Amol type="mRNA" |
| Amol type="mRNA" |
| Cultivar="BMS (Black Mexican Sweet)" |
| Ab_xref="taxon:4577" |
| About type="suspension culture" |
| About type="mixed logarithmic and stationary growth phases" |
| About the type |
| About the type="mixed logarithmic and stationary growth phases" |
| About the type="mixed logarithmic and stationary growth phases" |
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AI738207.1
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Matches 28
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VERSION
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                             AUTHORS
TITLE
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COMMENT
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nwvoly62
687009G02.x1 687 - Early embryo from Delaware Zea mays CDNA, mRNA
sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 628)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 599)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: immature ear; Vector: pBK-CMV; Site_1:
EcoRI; Site_2: XhoI; Mixed ear tissue cDNA library from
Schmidt lab"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XLOLR (Stratagene)"
/clone_lib="606 - Ear tissue cDNA library from Schmidt
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Maize ESTs from various CDNA libraries sequenced at Stanford
University
                                                                                                                   Stanford
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                                                                                 Walbot,V.
Maize ESTs from various cDNA libraries sequenced at
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                                                                                                                                                                                                Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 279.8; DB 1;
Pred. No. 9.5e-75;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                       Plate: 606047 row: B column: 11.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Zea mays"
mol type="mRNA"
cultivat="Ohio43"
db xref="taxon:4577"
tissue_type="mixed"
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Inbrary was prepared by George Rudenko using poly (A) learner RNA and Universal Ribocione CDNA Synthesis System elected RNA and Universal Ribocione CDNA Synthesis System (Promega). CDNA was synthesized using both random and oligo (AT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-dispeated pUCI9 vector. Blue/white salection on carbenicillin-containing plates was used to recover
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952032009.y2 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.
BQ163007.1 GI:20300064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNN)".
                                                                                                                                                                                                                                                                                                                                                                                                                                'dev_stage="mixed logarithmic and stationary growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 GCATTITACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA 291
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                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/oulfivar="mBNA" (Black Mexican Sweet)"
/db xref="taxon.4577"
/tissue_type="suspension culture"
                                                                                          Department of the control of column: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 276.8; DB 3;
Pred. No. 6.8e-74;
0; Mismatches 7;
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  University
Univolished (1999)
Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                               1. .290
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'lab host="DH10B"
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Best Local Similarity 97.6%;
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. col; SoLR"
/clone_lib="687 - Early embryo from Delaware"
/clone_lib="687 - Early embryo from Delaware"
/note="organ: embryo; Vector: pBluescript SK; Site 1:
XhoI; Site 2: EcoRI; Library was prepared by Statagene
using the Uni-ZAP XR system (Stratagene BN93728-12).
Clones were picked by bob after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
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    (bases 1 to 290)

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952077G01.y3 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays CONA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA
                                         Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbockestanford.edu
Plate: 687009 row: G column: 02.
                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/tissue_type="embryo"
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/organism="Zea mays"
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                         Contact: Walbot V
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Expressed Sequence Tags from B73 Maize Shoot Apical Meristems Unpublished (2004)
   Panicoideae; Andropogoneae; Zea
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Location/Qualifiers
                                                                                                                                                                                                                                                                                            /organism="Zea mays"
/mol_type="mRNA"
/cultivar="Ohio43"
                      (bases 1 to 461)
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Matches 282; Conservative
                                                                        University
Unpublished (1999)
                                                                                                              Contact: Walbot
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced TRNN))"
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                                                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
Walbot, V.
Maize ESTB from various cDNA libraries sequenced at Stanford
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                              University
University
Unpublished (1999)
Contact: Walbot:
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952032 row: D column: 09.
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Chen, H.D., Zhang, X., Zhou, R.L., Arias L, A.C., Shendelman, J.M.,
Zazubovits, N., Borsuk, D.A., Emrich, S.J., Ashlock, D.A., Scanlon, M.J.
and Schnable, P.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="660 - Mixed stages of anther and pollen"
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Site_2: XhOI; Anther and pollen cDNA library.
Directionally sequenced with 5' end at the EcoRI site.
Created by Amie Franklin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 AGCCGGCTTTATGTGCCTAGAAACTAGTAGCTAGTGGTGGTTGCTGCTGTGTGAATGACACTAT
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MESTROO E04.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
DN217785
DN217785.1 GI:60350812
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                                                                                                                                                         Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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Query Match
Best Local Similarity 98.6
Matches 273; Conservative
                                                                                                 DN223533.1
                                                                                                                            Zea mays
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leaf primordia staged Pl-P4"
/lab_host="XL1-Blue"
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Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
7015B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
781: 515-294-0975
Fax: 515-294-5256
Email: Schnable@lastate.edu.
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Pred. No. 5.5e-72;
0; Mismatches 4;
                                                                                                                                      /mol_type="mRNA"
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                                                                                                                        organism≂"Zea mays"
                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.6%;
Matches .273; Conservative
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MEST1144_E03.T7-1 UGA-ZmSAM-XZ2 Zea mays CDNA, mRNA sequence.
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Chen, H.D., Zhang, X., Zhou, R.L., Arias L, A.C., Shendelman, J.M.,
Zazubovits, N., Borsuk, L.A., Emrich, S.J., Ashlock, D.A., Scanlon, M.J.
and Schnable, P.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged Pl-P4"

| Jab_host="XL1-Blue" |
|/clone lib="Udga-ZmSAM-XZ2" |
|/clone lib="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1:
| BcoRI; Site_2: XhoI; This library was constructed by Raolan Shang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged Pl-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice
                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                               Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
Unpublished (2004)
Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence. For reasons that are not understood many clones in this library lack an XhoI site at their 3' ends."
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                                                                                                                                                                                                                                                                                                                                                                          Schnable Laboratory

Iowa State University

2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975

Fax: 515-294-5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="inbred B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: schnable@iastate.edu.
Location/Qualifiers
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                                                                GI:60356560
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1 14 61 74 72 121 134 194 241	AGCCGGCTTTATGTGCGTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT 60 	GCAATGRGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCGGTAA 120 	AAITIGGGGGCTCCCCGTAIGAGAIGCTGCGGGCAAGGCCTCGGTGTCCCACCTCGTTT 180	GIGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGAAGCCCTTTAAACTGTTGTCA 240	CTIGCAITITACCTITICCAICGCIGITIAIIGIGAG 277 	
		61 GCAAT 74 GCAAT	121 AATTT 134 AATTT	181 GTGGC 194 GTGGC	241 CTTGC 254 CTTGC	

Search completed: March 8, 2006, 05:42:27 Job time : 2340.81 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 16359, A Sequence 16362, A Sequence 16471, A Sequence 16130, A Sequence 16089, A 27361, A 149636, Sequence 5398, Ap Sequence 17140, A Description Sequence (Sequence Sequence Sequence Sequence Sequence S-09-252-91A-16130 S-09-952-91A-16130 S-09-949-016-14089 S-09-949-016-17958 S-09-949-016-13153 S-09-949-016-13153 S-09-949-016-13153 S-09-949-016-239 S-09-949-016-2361 09-949-016-150193 09-902-540-6363 09-949-016-15946 09-949-016-4204 SUMMARIES Query Match Length DB 1469 75378 12787 516 846 601 7381 25230 435 3798 3839 156942 156950 1023 1158 103377 29.8 29.8 29.8 Result 0000000

413, App

-09-902-540-413

Sequence 15964, A Sequence 13, Appl Sequence 33, Appl Sequence 13798, A Sequence 13798, A Sequence 15681, A Sequence 124, App Sequence 124, App Sequence 11892, A Sequence 11892, A Sequence 11875, A Sequence 15664, A Sequence 15664, A Sequence 1564, A Sequence 2094, A Sequence 262, Appli Sequence 4, Appli	ASSOCIATED OF DETECTION AND USES THEREOF	ength 1469; Indels 0; Gaps 0;	CTCCCCGTATGAGATGCTGCCG 152 CTCTCCAGGGAGGATGATGACC 92	39886CCGGTCTGGTTG 212 		
18 3 US-09-949-016-15964 152 2 US-09-252-991A-13905 162 6 PCT-USS5-0591A-13905 163 10S-09-255-0591A-13545 164 3 US-09-252-991A-13545 165 3 US-09-949-016-16951 165 3 US-09-949-016-11691 167 3 US-09-949-016-11891 168 3 US-09-949-016-11803 168 10S-09-949-016-11803 169 10S-09-949-016-11759 169 3 US-09-949-016-11759 169 3 US-09-949-016-11759 169 3 US-09-949-016-12514 168 3 US-09-949-016-12514	ALIGNMENTS al. SMS IN KNOWN GENES IN DISEASE, METHODS (709/949,016 114 41,755 37,768 31,498 Version 4.0	; Score 34.6; DB 3; Length ; Pred. No. 0.15; 0; Mismatches 54; Indels	CGACGCTAGTTATGACTGTCGCTCAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCG 	GGCAAGGCCTCGGTGTCCCACCTCGTTTGTGGCGGGGGGGCGCTGGAGCCCGGTCTGGTTG 		,/09949016
2 90618 2 1062 2 2 1065 2 2 1065 3 2 1656 3 2 8025 3 3 1 5732 3 1 5732 3 1 5732 3 0 15164 3 0 15164 3 0 100468 3 0 100468 3 0 100468 3 0 100468 3 1 1449 3	: 11cation US/0 N: 7. Craig et N: POLYMORPHI N: WITH HUMA N: WITH HUMA N: WITH HUMA N: WITH HUMA N: WITH HUMA N: 2000-04- 1 NUMBER: 60/2 1 NUMBER: 60/2 1: 2000-10-03 1: 2000-10-03 1: 2000-09-08 NUMBER: 60/2 1: 2000-10-03 1: 2000-10-03 1: 2000-09-08 NOS: 207012	11.9% larity 55.4% Conservative	ragitatgaci 	SCCTCGGTGTC CCTGAAGGAC		:-17140/c 1140, Application US/09949016 6812339 °ORMATION:
29.68 29.66 29.66 29.66 29.66 29.76 29.76 29.77 29.78 29.79 29.70 29.70 29.70 29.70 29.70 29.70 29.70 29.70 29.70 29.70 29.70 20.70	TLT 1 9-949-016-5398/c quence 5398, App tent 0. 6612339 NERAL INFORMATION 1TLE OF INVENTION 1TLE OF INVENTION 1TLE OF INVENTION THER REPERENCE: CI URRENT APPLICATION RIOR PILING DATE: RIOR APPLICATION RIOR FILING DATE: RIOR PILING DATE: RIOR PILING DATE: RIOR PILING DATE: RIOR FILING DATE: RIOR FILING DATE: RIOR FILING DATE: RIOR FILING DATE: LENGTH: 1469 Q ID NO 5398 LENGTH: 1469 Q ID NO 5398 TYPE: DNA ORGANISM: Human 9-949-016-5398	atch sal Simi 67;	93 CGACGCT 151 CAAGGCC	153 GGCAAGC 91 GTGGCCC	213 G.213 31 G 31	4 H 2
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-949-0 Sequence Sequence GENERAL IN TITLE OF TITLE O	Query Ma Best Loo Matches	& 8	රු සි	& 8	RESULT 2 US-09-949-016 ; Sequence 17 ; Patent No. ; GENERAL INF

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Sequence 16362, Application US/09252991A

Sequence 16362, Application US/09252991A

Sequence 16362, Application US/09252991A

Sequence 16362, Application US/09252991A

SERVERAL INFORMATION:

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

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LENGTH: 516
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Sequence 16471, Application US/09252991A

Sequence 16471, Application US/09252991A

Patent No. 6551795

Trib of INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: ARGUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ASKUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FAPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 946
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                                                   188 GGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCTTTAAACTGTTGTCACTTGCAT 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 CCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAAAATTTGGGGGCTCCCC
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US-09-252-991A-16471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16362
                                                                                                                                                                                                                     248 TTTACCTTTTCCATCGCTGTTT
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53.1%;
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ilarity 53.1%;
Conservative 0
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Best Local Similarity
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Best Local Simi:
Matches 69;
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JITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

JITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

JITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16359

LENGTH: 12787
## APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PPLICATION NUMBER: 60/241,755

PRIOR PPLICATION NUMBER: 60/241,755

PRIOR PPLICATION NUMBER: 60/237,768

PRIOR PPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 17140

LENGTH: 75378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 CGACGCTAGTTATGACTGTCGTCAGTAAAATTTGGGGGGCTCCCCGTATGAGATGCTGCCG
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Best Local Similarity 55.4%; Pred. No. 1.2;
Matches 67; Conservative 0; Mismatches 54; Indels 0;
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11.4*; Score 33.2; DB 3;
Best Local Similarity 52.1*; Pred. No. 1.5;
Matches 74; Conservative 0; Mismatches 68;
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i LOCATION: (1)...(75378)
i OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17140
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ORGANISM: Human
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ORGANISM: Human
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US-09-949-016-177958/c

Sequence 177958, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VEWTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: 05/949,016

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 TGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCCACCTCGTTTGTGG 184
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                                                                                                                                                                                                                                                                                                               Gape
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                                                                                                                                                                                                                                                                                                          37; Indels
                                                                                                                                                                                                                                                        Score 31.8; DB 3;
Pred. No. 14;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73198 radaacrreserareresecasesasaresr 73228
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Pred. No. 2;
0; Mismatches
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SOFTWARE: PastSEQ for Windows Version 4.0
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Patent No. 6812339
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PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                      ; LOCATION: (1)...(103377)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14089
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 59.3%;
Matches 54; Conservative
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                                                                                                  FEATURE:
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Best Local Similarity
Matches 62; Conserv
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; ORGANISM: Human
US-09-949-016-177958
                                                         TYPE: DNA
ORGANISM: Human
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                               103377
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       SEQ ID NO 14089
LENGTH: 10337
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GENERAL INFORMATION: NUCLEIC AID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: AUGUST: 107166.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
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                                                 77 CCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAAAATTTGGGGGCTCCCC 136
                                                                                                                                              137 GTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTTGTGGCGGGGGGGCGCTG 196
                                                                                               303 ccridegericcridececicecicirescricriccrideacaagacccrecriresresecae 362
                                                                                                                                                                                               363 cercéacceáriceráaceerasoaséanasoaceacerasasosimes de 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 CCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAAAATTTGGGGGCTCCCC
       0; Gaps
     Indels
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     61;
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Best Local Similarity 53.1%; Pred. No. 0.68;
Matches 69; Conservative 0; Mismatches 61;
     Mismatches
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6812339
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  Conservative
                                                                                                                                                                                                                                                                                                  423 GGGAGAGGGC 432
                                                                                                                                                                                                                                                   197 GAGCCCGGTC 206
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LENGTH: 885
: 69
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Matches
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Query Match
Best Local Similarity .69.5%;
Matches 41; Conservative
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US-09-621-976-15639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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US-09-949-016-27361
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                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Sequence 113153, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL3197

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-06

SOUTHARE: PREADER SECTION NUMBER: 60/231,498

NUMBER OF SECTION NOS: 207012

SOUTHARE: PREADER SECTION NOS: 207012

SEQ ID NO 13153

LENGTHREE
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                                                                                                                                                                                                                                                                                                                                                             10.6%; Score 30.8; DE
54.4%; Pred. No. 7.6;
tive 0; Mismatches
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FRANCE FOR WINDOWS VERSION 4.0
; SEQ ID NO 16844
; LENGTH: 7381
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US-09-134-001C-2640/C
Sequence 2640, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16844
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Best Local Similarity 63.9
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.4
Matches 62; Conservative
                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-01-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2640
LENGTH: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YRYSYMGYKMKSWSKKWKKYSGKWGTSKSTRKYRTYTSKCRKTTCKYRGWWSWKWRWWRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGTCTGGTTGGGAAGCCCTTTAAACTGTTGTCACTTGCATTTTACCTTTTCCA 260
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; Patent No. 6639063
; Reneral INPORMATION:
; APPLICANT: Johnst Mine Edwards, J.B.
APPLICANT: Johert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE OF INVENTION UNDERS: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
; SOFWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 GTTGGGTTGGGAAGCCCTTTAAACTGTTGTCACTTGCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30.2; DB 3;
Pred. No. 2.7;
0; Mismatches 18;
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Search completed: March 7, 2006, 23:09:18 Job time : 124.379 secs
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           TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION.
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Pred. No. 3.3;
0; Mismatches 28;
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Pred. No. 3.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 149636
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 09-949-016-149636
Sequence 149636, Application US/09949016
Application US/09949016
                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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Best Local Similarity 62.7%;
Matches 47; Conservative
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Best Local Similarity 62.7
Matches 47; Conservative
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; ORGANISM: Human
US-09-949-016-149636
                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-27361
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 27361
LENGTH: 601
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103 TATGACTGTCGTCAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCT 162
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                                                                                                                                            APPLICANT: Fechtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Pechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6300-11A
CURRENT APPLICATION NUMBER: US/09/311,021
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 901,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 CGGTGTCCCACCTCGTTTGTGCCGCGCGCGCCTGGAGCCCCGGTCTGG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587 IGAIGAGCICCCIGGGCIGAGGAGAGGGIGIICCAGGCCIGIGIGG 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30.2; DB
Pred. No. 4;
0; Mismatches
                       Application US/09311021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.1%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-311-021-91
-021-91
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 91
LENGTH: 901
TYPE: DNA
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March 8, 2006, 04:19:11; Search time 775:844 Seconds (without alignments) 865.410 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                        OM nucleic - nucleic search, using sw model
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1 agccggctttatgtgcgtag......tgtgagtggtcctatatcaa 291 IDENTITY NUC Gapop 10.0 , Gapext 1.0 US-10-603-524A-2 291 Title: Perfect score: Sequence: Scoring table:

15346750 Total number of hits satisfying chosen parameters: 7673375 segs, 1153648444 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:* ptodata/z/pubpna/PCT_NEW_PUB.seq:* Ptodata/z/pubpna/US09_NEW_PUB.seq:* Ptodata/z/pubpna/US09_NEW_PUB.seq1_ ptodata/z/pubpna/US10_NEW_PUB.seq1_ ptodata/2/pubpna/US06_NEW ptodata/2/pubpna/US07_NEW Published_Applications_NA_New: /cgn2_6/1 /cgn2_6/1 /cgn2_6/1 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			d			SUMMARIES	
Result	ult		Query				
	No.	Score	Match	Match Length DB	60	ID	Description
	-	183.2	63.0	1252	6	US-11-096-568A-16048	Sequence 16048. A
υ	7	33.4	11.5	599	9	US-09-925-065A-705105	Sequence 705105,
	m	32.8	11.3	201	12	US-11-124-367A-21598	Sequence 21598, A
U	4	32.6	11.2	553	9	US-09-925-065A-10284	Sequence 10284, A
υ	'n	32.6	11.2	553	9	US-09-925-065A-10285	Sequence 10285, A
υ	9	32.2	11.1	553	9	US-09-925-065A-10286	Sequence 10286, A
υ	7	31.4	10.8	959	9	US-09-925-065A-88099	Sequence 88099, A
U	80	31.2	10.7	3372	12	US-11-037-243-18	Sequence 18, Appl
	σ	30	10.3	266	9	US-09-925-065A-457896	Sequence 457896,
	10	30	10.3	629	9	US-09-925-065A-916170	Sequence 916170,
υ	11	30	10.3	634	9	US-09-925-065A-915272	Sequence 915272,
U	12	30	10.3	100000	12	US-11-124-368A-2913	Sequence 2913, Ap
υ	13	29.8	10.2	630	9	US-09-925-065A-788291	88291
υ	14	29.8	10.2	1149	9	US-09-925-065A-709944	Sequence 709944,
υ	15	29.8	10.2	1785	89	US-10-750-185-50507	Sequence 50507, A
υ	16	29.8	10.2	1785	αņ	US-10-750-623-50507	Sequence 50507, A
ű	11	29.6	10.2	7001	12	US-11-011-332A-75	Sequence 75, Appl
U	18	29.6	10.2	8252	12	US-11-011-332A-150	Sequence 150, App
U	13	29.5	10.0	446	9	US-09-925-065A-36828	Sequence 36828, A
U.	20,	29	10.0	608	9	US-09-925-065A-735119	Sequence 735119,

Sequence 813302,	Sequence 842902,	Sequence 2, Appli	Seguence 18466, A	Sequence 3, Appli	Sequence 361, App	Seguence 361224,	Sequence 213, App	213, 7	70994	Sequence 1901, Ap	Sequence 97, Appl			Sequence 4365, Ap		12499	Sequence 124992,	Sequence 124993,	Sequence 40044, A	Sequence 40045, A	Sequence 17, Appl	Sequence 811758,	Sequence 811760,	Sequence 848890,
US-09-925-065A-813302	US-09-925-065A-842902	US-10-522-037-2	2 US-11-124-367A-18466	2 US-11-121-086-3	US-10-802-796-361	US-09-925-065A-361224	US-10-750-185-213	US-10-750-623-213	US-09-925-065A-709945	US-10-793-626-1901	US-10-947-249-97	US-10-932-182A-4088	US-10-932-182A-4088	US-10-793-626-4365	US-10-330-773-211	US-09-925-065A-124990	US-09-925-065A-124992	US-09-925-065A-124993	US-09-925-065A-40044	US-09-925-065A-40045	US-11-121-086-17	US-09-925-065A-811758	US-09-925-065A-811760	US-09-925-065A-848890
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608	609	37507	201	168516	312	512	9	9	1149	1419	1510	1968	1968	2986	23877	604	604	604	1197	1197	178877	598	603	633
10.0	10.0	10.0	9.9	9.9	9.8	9.8	9.8	9.8	9.8	9.8	8.6	9.8	9.8	9.6	9.8	9.8	9.8	9.8	9.8	8.6	9.8	9.7	9.7	9.7
29	29	29	28.8	28.8	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.4	28.4	28.4	28.4	28.4	28.4	28.2	28.2	28.2
21	22	23	24	52	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

RESULT 1 US-11-096-568A-16048 j Sequence 16044, Application US/11096568A j Sequence 16044, Application Wo. US20060048240A1 j CENERAL INFORMATION: APPLICANT: Alexandrow, Nickolai et al. TILE OF INVENTION: Therby TILE OF INVENTION: Therby TILE REFERENCE: 2750-1592PUS2 CURRENT FAPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01 NUMBER OF SEQ ID NOS: 34471 SEQ ID NO 16048 LENGTH: 1252 TYPE: DNA ORGANISM: Zea mays subsp. mays FRAIDER: LOCATION: (1)(1252) OTHER INFORMATION: Ceres Seq. ID no. 12350354 US-11-096-568A-16048	Polypeptides
Query Match 63.0%; Score 183.2; DB 9; Length 1252; Best Local Similarity 81.0%; Pred. No. 8.5e-49; Matches 243; Conservative 0; Mismatches 43; Indels 14; Gaps 2;	2;
1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT	
935 AGCCGGCTTTACATGCCTAGAAGCTAGTACCTAGTGTTTGCTGCTGTCTAATGACATTAT	
61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGAGGCTAGTTATGACTGTC	
Db 995 GCAATGTGATCTGGACCCTGGTTTCTTGGGTGCGACGCTTGTAGCCGCCGTCTTATGATT 1054	
Qy 113GTCAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGCAAGGCCTCGGT 166	
Db 1055 ATTTGTCGGGAAAATTTGGGGGCTCCCCATATGAGATGCTGCCGGGGAAGACCTCGCCAT 1114	1114
Qy 167 GTCCCACCTCGTTTGTGGGGGGGGGCGCTGGAGCCCGGTCTGGGTTGGGAAGCCCT 226	
Db 1115 CCCCCACCTCGTTTCAGGCGGGGGACGCTGGTCCGGTTGGGTTGGGATGGGAAGCCCC 1174	1174

227 TTAAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286

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Query Match
Best Local S
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                                                                                                           TYPE: DNA
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1175 TTAAACTGTTGTCGCTTGCATTTTAACCTTTTCATCGCCCGTTCAGTGGTCCTAAATCTAT 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 526 GGTTCCTGGTGGGGGGGGGCCCCTGGATCTATGCTGAGAACATTATTCTTCTTGTGCCC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 CGCTAGTTATGACTGTCGTCAGTAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGC 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 AAGGCCTCGGTGTCCCACCTCGTTTGTGGCGGGGGGGCGCTGGAGCCCGGTCTGGTTGGGT 215
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Publication No. US20060024700A1

GENERAL INFORMATION:
APPLICANT: Michole Cargill
APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01519.0NB CORRENT APPLICATION NUMBER: US/11/124,367A
CURRENT PILING DATE: 2004-05-09
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR PLING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR APPLICATION NUMBER: US 60/599,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 GTTTGCTGCTGTCGAATGACACTATGCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                Sequence 705105, Application US/09925065A; Publication No. US20040181048A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
ITILE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
FRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
FRIOR APPLICATION NUMBER: US 60/252,147
FRIOR FILING DATE: 2000-11-30
FRIOR PILING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 96; Indels
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Pred. No. 1;
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Best Local Similarity 48.7
Matches 91, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-925-065A-705105
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59 AATGGAGGCGCTGCCGGACCCTCCCCCCAATCCCGMGTCGTCACCCCCTGCTT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAAAA 122
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                                                                                                                                                                                                                                                                                                                                                                                                          121 AATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTT
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| Sequence 10284, Application US/09925065A
| Publication No. US20040181048A1
| GRNERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single
| TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135
| CURRENT APPLICATION NUMBER: US/09/925,065A
| CURRENT PILING DATE: 2001-08-08
| PRIOR PILING DATE: 2000-10-24
| PRIOR FILING DATE: 2000-11-20
| PRIOR FILING DATE: 2000-11-20
| PRIOR PILING DATE: 2000-11-30
| PRIOR PILING DATE: 2000-11-30
| PRIOR PILING DATE: 2000-11-16
| PRIOR PPLICATION NUMBER: US 60/250,092
| PRIOR PILING DATE: 2001-11-16
| PRIOR PPLICATION NUMBER: US 60/261,766
| PRIOR PPLICATION NUMBER: US 60/261,766
| PRIOR PILING DATE: 2001-01-16
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
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Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                                                                               Score 32.8; DE Pred. No. 1.1; 1; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 21598
LENGTH: 201
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58.5%;
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Best Local Similarity 52.6%;
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                             l Similarity 58.5
55; Conservative
                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-124-367A-21598
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Query Match
Best Local Similarity
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Fublication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-11-20
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR APPLICATION NUMBER: US 60/289,846
FRIOR APPLICATION NUMBER:
IIILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome IIIR REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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Pred. No. 2.4;
1; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Indels
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Pred. No. 1.8;
0; Mismatches 64;
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PRIOR PELICATION NUMBER: US 60/243,096
PRIOR PELING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PREUSEQ for Windows Version 4.0
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52.6%;
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Past Local Similarity 51.9%;
Matches 70; Conservative
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Best Local Similarity 52.6
Matches 71; Conservative
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US-09-925-065A-10285
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US-09-925-065A-10286
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LENGTH: 553
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3 CCGCCTTTATGTGCGTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTATGC 62

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236 CCTACTTIGTAAGCCATAACTCCTGGGTCTCTTGGGTTCTAATGACCCRGGAGACTCTTC 177
                                                                                                              63 AATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCGTAAAA 122
                                                                                                                                                                                 176 AArgacArriggArrcrigrrirccriggGagCrrrcriccriAArccriggGarAcricAAA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827,135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2000-10-28
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-46
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-10
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Pred. No. 4.7
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CURRENT FILING DATE: 2005-05-26
PRIOR APPLICATION NUMBER: US/09/888,615
PRIOR FILING DATE: 2001-06-26
PRIOR PAPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
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; Sequence 88099, Application US/09925065A
; Publication No. US20040181048A1
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APPLICANT: CARNEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARGANDM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REPERENCE: 038602/1214
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Publication No. US20050287546A1
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APPLICANT: PLOWMAN, GREGORY
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US-09-925-065A-88099
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Sequence 457896, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICATY: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT FILING DATE: 2001-08-08

PRIOR PPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2001-11-30

PRIOR FILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-05

SEQ ID NO 457896

LENGTH: 566
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                                                                                                                                                                                                                                  Length 3372;
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13;
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                                                                                                                                                                                                                                                                                                                                                                                  10.7%; Score 31.2; DB 12; 57.0%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 43;
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Best Local Similarity 57.4%; Pred. No. 3
Matches 54; Conservative 0; Mismatch
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 3372
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Matches 57; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-457896
                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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US-09-925-065A-916170
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Fublication No. US20040181048A1
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Indentification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
FRIOR PELICATION NUMBER: US 60/243,096
FRIOR PELICATION NUMBER: US 60/251,147
FRIOR PELICATION NUMBER: US 60/252,147
FRIOR PELICATION NUMBER: US 60/250,092
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR APPLICATION NUMBER: US 60/261,766
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10.3%; Score 30; DB 6
Best Local Similarity 53.4%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

SOFTWARE: FREUSED FOR WINDOWS VETSION 4.0

SEQ ID NO 916170
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US-09-925-065A-915272
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US-09-925-065A-915272/c
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Pred. No.

us-10-603-524a-2.rnpbn

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Best Local Similarity 55.2%;
Matches 58; Conservative
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Best Local Similarity
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SEQ ID NO 709944
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                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01524
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US /11/124, 368A
PRIOR APPLICATION NUMBER: US 60/568, 845
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PELING DATE: 2000-11-30

PRIOR PELING DATE: 2001-01-6

PRIOR PELING DATE: 2001-01-6

PRIOR PELING DATE: 2001-01-6

PRIOR PELING DATE: 2001-01-6

SEQ ID NO 788291

LENGTH: 630

TUBLES OF THE THING DATE: 2001-05-09

NUMBER: OF SEQ ID NOS: 957086

SEQ ID NO 788291

LENGTH: 630
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Pred. No. 79;
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2913
LENGTH: 100000
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PRIOR FILING DATE: 2004-11-09
                                                                                                                       Sequence 2913, Application US/11124368A
Publication No. US20050287559A1
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ORGANISM: Homo sapiens
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GORGANISM: Homo sapiens
US-Ü9-925-065A-788291
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Matches 66; Conserva
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10.2%; Score 29.8; DB 6; Length 630;

Query, Match

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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PLLING DATE: 2000-10-24
PRIOR PLLING DATE: 2000-11-20
PRIOR PLLING DATE: 2000-11-20
PRIOR PLLING DATE: 2000-11-30
PRIOR PLLING DATE: 2000-11-6
PRIOR PLLING DATE: 2001-11-6
PRIOR PLLING DATE: 2001-01-6
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APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                      63 AATGIGATCIGGAACCIGGITTCITGGGIGCGACGCIAGTIAIGA 107
                                                                                                                                                                                                                                                                                                 448 Acrcrigarciraaacrgccirircrggagrgcrragaraaggaraa 404
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ed. No. 15;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 709944, Application US/09925065A
Publication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50507, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
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APPLICANT: DENISE; Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64; Conservative
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US-09-925-065A-709944
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0; Gaps
                                                                                                                                                                                                                    Query Match 10.2%; Score 29.8; DB 8; Length 1785; Best Local Similarity 60.5%; Pred. No. 22; Matches 49; Conservative 0; Mismatches 32; Indels 0;
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 50507
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Bovine 19866880889331
US-10-750-185-50507
                                                                                                                                                                                                                                                                                                                                                                            162 TCGGTGTCCCACCTCGTTTGT 182
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Search completed: March 8, 2006, 06:10:11 Job time : 776.844 secs

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8, 2006, 04:11:07; Search time 629.177 Seconds (without alignments) 3824.664 Million cell updates/sec
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/ Cgn2 6/ptodata1/pubpna/US08 PUBCOMB.seq:*
/ Cgn2 6/ptodata1/pubpna/US08 PUBCOMB.seq:*
/ Cgn2 6/ptodata1/pubpna/US09B PUBCOMB.seq:*
/ Cgn2 6/ptodata1/pubpna/US10B PUBCOMB.seq:*
/ Cgn2 6/ptodata1/pubpna/US10B PUBCOMB.seq:*
/ Cgn2 6/ptodata1/pubpna/US10B PUBCOMB.seq:*
/ Cgn2 6/ptodata1/pubpna/US10C PUBCOMB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9793542 seqs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_NA_Main:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
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291
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seg:*

					SUMMARIES		
Result		* Ouery			*		
No.	Score	Match	Match Length DB	DB	QI	Description	
	291	100.0	291	7	US-10-603-524A-2	Sequence 2. Appli	
7	285.8	98.2	653	7	US-10-425-114-19731		
e	285.8	98.2	1283	7	US-10-425-114-21156		
4	260.2	89.4	733	7	US-10-425-114-32231		
2	258.2	88.7	689	7	US-10-425-114-20758		
9	253.2	87.0	752	7	US-10-425-114-32479		
7	245.8	84.5	487	7	US-10-425-114-17184		
80		76.1	267	7	US-10-424-599-14742		
6	2	75.1	394	æ	US-10-425-115-6597	_	
10	217	74.6	1270	7	US-10-767-701-15432		
11	206.2	70.9	464	80	US-10-425-115-153129		
12	195.2	67.1	807	7	US-10-425-114-15469	٠.	
13		67.1	824	7	US-10-425-114-25681		
14		67.1	696	7	US-10-425-114-26656		
15	195.2	67.1	1114	œ	US-10-425-115-6593	Sequence 6593, Ap	
16	189.6	65.2	283	œ	US-10-425-115-76283		
c 17	177.2	6.09	383	œ	US-10-425-115-119075		
c 18	172.2	59.5	378	80	US-10-425-115-14719		
c 19	172.2	59.2	394	80	US-10-425-115-123144		
c •20	170.2	58.5	385	œ	US-10-425-115-162596		
c 21	163.8	56.3	219	œ	US-10-425-115-70427	Sequence 70427, A	
c 22	160.2	55.1	303	œ	US-10-425-115-147735	٠.	
23	159.6	54.8	361	80	US-10-425-115-119871		

Sequence 90459, A Sequence 31651, A Sequence 158692, Sequence 60002, A		Sequence 110313, Sequence 24201, A Sequence 166630, Sequence 160256,		
US-10-425-115-90459 US-10-425-115-31651 US-10-425-115-158692 US-10-425-115-60002	US-10-425-115-5993 US-10-425-115-158411 US-10-425-115-6598 US-10-425-115-145527	US-10-425-115-110313 US-10-425-115-24201 US-10-425-115-166630 US-10-425-115-160256 US-10-425-115-160256	US-10-425-115-149447 US-10-425-115-148802 US-10-425-115-95269 US-10-425-115-164467 US-10-425-115-15414	US-10-425-115-64669 US-10-425-115-6255 US-10-425-115-85267 US-10-425-115-183855
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157.2 153.4 145.2 143.6	112.2 111.4 111.2 110.8	110.8 109.2 106.6 105.6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	84.4 76.2 69.8 69.2
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ALIGNMENTS

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        Sequence 2, Application US/10603524A

Publication No. US2004015887A1

GENERAL INFORMATION:

APPLICANT: DOW ASTOSCIENCES LLC

ITLLE OF INVENTION: USE OF REGULATORY SEQUENCES IN TRANSGENIC PLANTS

CURRENT APPLICATION NUMBER: US/10/603,524A

CURRENT APPLICATION NUMBER: 05/392571

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-27

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 291
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Best Local Similarity 100.
Matches 291, Conservative
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US-10-603-524A-2
US-10-603-524A-2
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RESULT

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Score 285.8; DB 7;
Pred. No. 3.6e-85;
0; Mismatches 2;
   98.2%;
99.3%;
                           Best Local Similarity 99.3 Matches 287; Conservative
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Matches 283; Conservative
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ORGANISM: Zea mays
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; Sequence 21156, Application US/10425114
; Publication No. US2004003488BA1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Screen, Steven E
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, 
                                              GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Sorien, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53313) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 19331
LENGTH: 653
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98.2%; Score 285.8; DB 7
Best Local Similarity 99.3%; Pred. No. 2.8e-85;
Matches 287; Conservative 0; Mismatches 2
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COTHER INFORMATION: Clone ID: LIB3279-175-F1_FLI US-10-425-114-21156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: LIB3150-117-G4_FLI US-10-425-114-19731
   Sequence 19731, Application US/10425114
Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
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ORGANISM: Zea mays
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Sequence 32231, Application US/10425114

Sequence 32231, Application US/10425114

Sequence 32231, Application US/004003488A1

SEQUENCE 10. US2004003488A1

SERENZAL INFORMATION:

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Soreen, Serven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128
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                                                                                                                                          Indels
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Matches 247; Conservative
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Best Local Similarity
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ORGANISM: Zea mays
      ORGANISM: Zea mays
                                                                                               US-10-425-114-32479
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APPLICANT: Soreen, Yahua

APPLICANT: Soreen, Serven E

APPLICANT: Tabaska, Jack E

APPLICA
                                                                                                                                                                                                                                                                 APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE STERENCE: 38-21(5313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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   TGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA 694
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US-10-425-114-20758
                                                                                                                                                 Sequence 20758, Application US/10425114
Ublication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 20758
LENGTH: 689
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APPLICANT: Screen, Steven B
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US, 10/425, 114
CURRENT APPLICATION NUMBER: US, 10/425, 114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
LENGTH: 487
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                                                                                                                                                                                                                                                            461 AGCCGGCTTTATGTGCCTAGAAACTAGTAGCTAGTGTTTGCTGCTGCTGCTGCAATGACACTAT
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Pred. No. 7e-72;
0; Mismatches 2; Indels 0
                                                                                           Length 752;
                                                                                                                                                          Indels
                                                                 Score 253.2; DB 7;
Pred. No. 2.7e-74;
OTHER INFORMATION: Clone ID: UC-ZMFLB73376G05_FLI
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US-10-425-114-17184
                                                                                        Query Match
87.0%; Score 253.2;
Best Local Similarity 94.5%; Pred. No. 2.7e
Matches 276; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-425-114-17184
Sequence 17184, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 84.5%;
99.2%;
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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9 85

Gaps

10;

Indels

Length 394;

172

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Sequence 15432, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Winha
APPLICANT:
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 15432
LENGTH: 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 TGTTGTCACTTGCATTTTACCTTTT-CATCGCTGTTTATTGTGAGTGGTCCTAAATCAA 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS49_330
US-10-767-701-15432
                                                                                                                                                                     Score 218.6; DB 8;
Pred. No. 9e-63;
0; Mismatches 19;
                                   ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106008C.1
US-10-425-115-6597
                                                                                                                                                                     Query Match 75.1%;
Best Local Similarity 90.3%;
Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Sorghum bicolor
   ORGANISM: Zea mays
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JUSTICAL 25-115-6597

JUSTICAL INFORMATION

                                                                                                                                                                                                                                                                                      Sequence 14742, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: Can Vondwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 288684
SEQ ID NO 14742
LENGTH: 267
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419 GTGGCGGGGGGCGCTGGAGCCCGGTCTGGTTGGGAAGCCCTTTAAACTGTTGTCA 478
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US-10-424-599-14742
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                                                                                                             479 CTTGCATTT 487
                                                                      241 CTTGCATTT 249
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                                                                                                                                                                                                                                                                            -10-424-599-14742
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TYPE: DNA
ORGANISM: Zea mays
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Publication No. US20040034888A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: About, Yihua
APPLICANT: About, Yihua
APPLICANT: Cac, Yongwel
APPLICANT
                                                                                                                                                                                                                                                                                APPLICANT: La Rosa; Thomas J.
APPLICANT: La Rosa; Thomas J.
APPLICANT: La Rovalic, David K.
APPLICANT: Shou, Yinhad
APPLICANT: Shou, Yinhad
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT FILING DATE: 2003-04-28
SURBENT FILING DATE: 2003-04-28
SEQ ID NO 153129
LENGTH: 464
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412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 AAATTTGGGGTGCTCCCCACATGAGATGCTTCCGTACAAGGCCTCGCTGACCACCTCGC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 TGCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 AAATTTGGGG-GCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 TIGIGGGGGGGGCGCTGGAGCCCGGTCTGGTTGGGAAGCCCTTTAAACTGTTGT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCCGCCTTTATGTGC-GTAGAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.9%; Score 206.2; DB 8; Best Local Similarity 86.3%; Pred. No. 1.4e-58; Matches 251; Conservative 0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: MRT4577_71235C.1
US-10-425-115-153129
                                                                                                                                                                                                    Sequence 153129, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                         10-425-115-153129
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US-10-425-114-15469
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Sequence 25681, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Schou, Yihua
APPLICANT: Schou, Yihua
APPLICANT: Screen, Seeven E
APPLICANT: Tabaska, Jack E
APPLICANT: Car, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 GCAATGTGATCTGGACCCTGGTTTCTTGGGTGCGACGCTTGTAGCAGCCGTGTTATGATT 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  609 ATTIGLICGGAAAATTIGGGGGCTCCCCATAIGAGATGCTGCCGGGCAAGACTCTCGGCAT 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 GCAATGTGATCTGGACCCCTGGTTTCTTGGGTGCGACGCTTGTAGCAGCGGCGTGTTATGATT 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                                                                                                                                                                                                                                                                                                                                        489 AGCCGGCTTTACGTGCCTAGAAGCTAGTACCTAGTGTTTGCTGCTGTCTAATGACACTAT
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                                                                                                                                    Score 195.2; DB 7; Length 807;
Pred. No. 8.6e-55;
0; Mismatches 43; Indels 12;
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; PEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-005-C4_FLI
US-10-425-114-15469
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US-10-425-114-25681
                                                                                                                             Query Match 67.1%;
Best Local Similarity 81.5%;
Matches 243; Conservative
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US-10-425-115-6593
i Sequence 6593, Application US/10425115
i Publication No. US20040214272A1
i GENERAL INFORMATION:
i APPLICANT: La Rosa, Thomas J.
i APPLICANT: Zhou, Yihua
i APPLICANT: Cao, Yongwei
i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
i TITLE OF INVENTION: Nucleic Acid Molecules
i TITLE Acid Molecules
i T
                                                                                                                                                                                                                                           Sequence 26656, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Carou, Yihua

APPLICANT: Carou, Yihua

APPLICANT: Carou, Yihua

APPLICANT: Carou, Yongwel

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NOS: 73128

SEQ ID NO 26656

IENGTH: 969
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229 AAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
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Best Local Similarity 81.5%; Pred. No. 9.2e-55;
Matches 243; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: LIB4570-004-Al0_FLI
US-10-425-114-26656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                    1 AGCCGGCTTTATGTGCGTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT
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                                                                                                                                                                                                                                                     Indels 12;
                                                                                                                                                                                          Length 1114;
                                                                                                                                                                                    Query Match 67.1%; Score 195.2; DB 8; Best Local Similarity 81.5%; Pred. No. 9.6e-55; Matches 243; Conservative 0; Mismatches 43;
; TYPE: DNA
; ORGANIEM: Zea may8
; PEATURE:
; PEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106001C.1
US-10-425-115-6593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: March 8, 2006, 05:20:28
Job time : 630.177 secs
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Acres 1015 Breast ca Adv34981 Murine cD Abv31301 Human pro Abk31761 DNA encod Abq75958 Human PMM Ady47968 Human PMM Ady17184 Streptomy Add17186 Streptomy Adc19187 Plant cDN Acc25640 Prokaryot

Aca2826 Prokaryot
Adg59461 Human can
Ada13790 Murine ca
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Adq4818 Oligonucl
Abq1873 Oligonucl
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Abq16314 Oligonucl
Abq16315 Oligonucl
Abq50428 Oligonucl
Adg64183 Human can
Ac12346 Rice ablo
Adt20151 Plant cDN
Ad63136 Novel hum

Nav38365 Mouse ESX

score:

Sequence:

1

OM nucleic

Run on:

Scoring table:

Total number

Database

Searched:

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This sequence represents a 3' untranslated region (UTR) which was used in the construction of the recombinant expression cassette of the invention. The expression cassette is for effecting expression of a foreign gene in a transformed plant and comprises a promoter operable in plants, an untranslated leader sequence, a foreign gene of interest, and a 3'UTR. This cassette may be used to transform plants, for genetic engineering of plants or in improving the expression of transgenes in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated DNA molecule useful for genetic engineering of plants or for improving the expression of transgenes in plants, particularly corn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; 3' untranslated region; UTR; expression cassette; transformed plant; promoter; untranslated leader sequence; genetic engineering.
                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                        ACL32346
. ADT20151
ADQ63136
ACN83015
ADV34981
ABV51301
ABK31761
                                                                                                                                   ADQ59461
ADZ13790
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ABQ44819
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ADT19187
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ACA25826
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                                                                                                                                                                                                                                                                                                                                                                                                             ADI22023 standard; DNA; 291 BP
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 WO2004003177-A2.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Abd17758 Pseudomon Abd17867 Pseudomon Abd17526 Pseudomon Abv56992 Human pro

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                  Sequence 291 BP; 50 A; 63 C; 87 G; 91 T; 0 U; 0 Other;
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                                                       Score 291; DB 12;
Pred. No. 7.7e-86;
                                                                                           Mismatches
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05-NOV-2001; 2001US-00985678.
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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the Us patent of file at the program of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme cosmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 285.8; DB 13;
Pred. No. 5.7e-84;
); Mismatches 2;
Claim 1; SEQ ID NO 19731; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADX46416 standard; cDNA; 1283 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.2%;
ilarity 99.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2005 (first entry)
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Plant full length insert polynucleotide segid 32231.

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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance, heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; se.
                                                                                                                                                                                                                                                                                                                                      28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2001; 2001US-00985678.
                                             21-APR-2005 (first entry)
                                                                                                                                                                                                                                                                            US2004034888-A1
                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu J,
   The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the polymucleotide consisting of a sequence encoding an amino acid sequence to sequence. The US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme camporate participation of the cell cycle pathway, for conferring increased resistance to plant disease, for manipulating growth rate in lighth or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert of the increase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1055 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTTATGACTGTCGTCGTAA 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1175 Greecedececerceaececegrerecricerreserreseaasecerriaaacrerrere 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                       New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          995 AGCCGGCTTTATGTGCCTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGCCGGCTTTATGTGCGTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AATTIGGGGCTCCCCGTAIGAGAIGCTGCCGGCCAAGGCCTCGGTGTCCCACCTCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1115 AATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGCGGGGGCGCTGGAGCCCCGGTCTGGTTGGGAAGCCCTTTAAACTGTTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 285.8; DB 13; Length 1283;
Pred. No. 7.5e-84;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                  Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1283 BP; 287 A; 333 C; 369 G; 294 T; 0 U; 0 Other;
                                                                                                                                                                                                  Tabaska JE,
                                                                                                                                                                                                Screen SE,
                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 21156; 15pp; English.
                                                                                                                                                                                                Kovalic DK,
               28-APR-2003; 2003US-00425114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.2%;
99.3%;
                                            99US-00304517
                                                          05-NOV-2001; 2001US-00985678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 99.3
Matches 287; Conservative
                                                                                                   ZHOU Y.
KOVALIC D K.
SCREEN S B.
TABASKA J E.
                                                                                                                                                                                                                            WPI; 2004-180133/17.
                                                                                                                                                                                                Zhou Y,
                                                                                                                                                                                                                                                                                                       improving yield.
                                                                                                                                                                CAO Y.
                                            06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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                                                                                                                                                  (TABA/)
(CAOY/)
                                                                                                                    (KOVA/)
(SCRE/)
                                                                                                                                                                                              Liu J,
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Cao

Tabaska JE,

Screen SE,

Kovalic DK,

Zhou Y,

KOVALIC D K. SCREEN S E.

LIU J. ZHOU Y.

(/min/)

06-MAY-1999;

19-FEB-2004.

TABASKA J E

CAO Y.

(TABA/) (CAOY/)

SCRE/)

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the sequence. Lumi7Doc102004014888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pesses, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease. For producing galactomannan, ignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photocognythesis or carbohydrate, nitrogen or phosphorus use and/or uptake crease condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 AGCCGGCTTTATGTGCCTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                          New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 260.2; DB 13; Length
Pred. No. 1.8e-75;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 32231; 15pp; English.
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94.6%;
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WPI; 2004-180133/17.
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ò 셤 ò 셤 ઠે 셤 ઠ 셤 ò ADX61388 standard; cDNA; 733 BP.

ADX61388 ID ADX6 RESULT 4

9

RESULT 5 ADX46018

Gaps

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112 512 172 572

632

us-10-603-524a-2.rng

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CCTCGTTTGTGGCGGGGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCTTTAAAC 232
plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increased said character of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTTGTCACTTGCATTTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGCCGGCTTTATGTGCGTAGAACTAGTAGTAGTTTGCTGTGCTGTCGAATGACACTAT
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                                                                                                                                                                                                                                                                                                                                   Score 258.2; DB 13; Length 689;
Pred. No. 8e-75;
0; Mismatches 8; Indels 8;
                                                                                                                                                                                                                                                                                     Sequence 689 BP; 143 A; 169 C; 195 G; 182 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant full length insert polynucleotide seqid 32479.
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05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                 Query Match 88.7%;
Best Local Similarity 94.6%;
Matches 281; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADX61636 standard; cDNA; 752
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(ZHOU/) ZHOU Y.
(KOVA/) KOVALIC D K.
(SCRE/) SCREEN S E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004034888-A1.
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                                                                                                                                                                                                                                              invention.
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Best Local S
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                                                                                                                                                                                                                                                                 635
                                                                           515
                                                                                                                         172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                      CCTCGTTTGTGGGGGGGGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCTTTAAAC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme
                                                                                                                                                                                                                                                                                                                TGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA 291
                                                                                                                                                                                                                                                                                                                                          TGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                            456 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTAGCCGTGTTATGACTGTC
                                                                                                                                                    GTCCGTAAAATTTGGGGGCTCCCCGTAAGGATGCTGCTGGCAAGGCATGCTGCCTCGGTGCTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant full length insert polynucleotide seqid 20758.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 20758; 15pp; English.
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05-NOV-2001; 2001US-00985678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADX46018 standard; cDNA; 689
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KOVALIC D K.
SCREEN S E.
TABASKA J E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pests, for confeimproving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHOU Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIU J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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(CAOY/)
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New

extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;

protein content; gene; ss

US2004034888-A1

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19-FEB-2004.

Unidentified,

28-APR-2003; 2003US-00425114. 06-MAY-1999; 99US-00304517, 05-NOV-2001; 2001US-00985678.

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polymicleolistic consisting of a sequence encounty an author evidence.

Yeavilable in electronic form from the US patent office at
ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polymucleotide
of the invention are also useful in physical arrays of molecules and as
plant breeding markers. The recombinant DNA construct is useful for
improving plant tolerance to cold, heat, drought, herbicides, extreme
osmotic conditions, pathogens or pests, for manipulating growth rate in
plant cells by modification of the cell cycle pathway, for conferring
increased resistance to plant disease, for producing galactomannan,
combination in plants, for improving yield by modification of
photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
or by providing improved plant growth and development under at least one
streams condition or for modifying seed oil or protein yield and/or
content. This sequence represents a plant full length insert
polymucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                              The invention describes a recombinant DNA construct comprising a polymuclocide consisting of a sequence encoding an amino acid sequence and included the consisting of a sequence.
                                                                                                                           New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCGGCTTTATGTGCGTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCGGCTTTATGTGCCTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTAGCCGTGTTATGACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCAGTAAAATTTGGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCCGGTGTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCGTAAAATTTGGGGGCTCCCCGTAAGGGATGCTGCCTGGCAAGGCCTCGGTGTCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 752;
                                                         Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 752 BP; 154 A; 190 C; 210 G; 198 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                         Tabaska JE,
                                                                                                                                                                                                                                                          The invention describes a recombinant DNA construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 253.2; DB 13;
Pred. No. 3.8e-73;
.....heg 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCT
                                                       Screen SE,
                                                                                                                                                                                                                      Claim 1; SEQ ID NO 32479; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADX34364 standard; cDNA; 487.BP
                                                      Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.0%;
llarity 94.5%;
Conservative
                                                                                          WPI; 2004-180133/17.
TABASKA J E.
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les 276; Conserv
                                                      Zhou Y,
                                                                                                                                                                  pests, for confeimproving yield
                     CAO
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(TABA/)
                   (CAOY/)
                                                      Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for 358 418 The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant calls by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for increasing the rate of homologous recombining in plants, for improving yield by modification of 298 180 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGAAGCCCTTTAAACTGTTGTCA 240 photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert 9 used in the recombinant DNA construct of the 299 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTTATGACTGTCGTCAGTAA AGCCGGCTTTATGTGCCTAGAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA AATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTT AGCCGCTTTATGTGCGTAGAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT Gaps recombinant DNA construct, useful for improving plant tolerance ö DB 13; Length 487; χ; Cao Sequence 487 BP; 99 A; 118 C; 143 G; 127 T; 0 U; 0 Other; Score 245.8; DB 13; Length Pred. No. 8.8e-71;); Mismatches 2; Indels Tabaska JE, Screen SE, Claim 1; SEQ ID NO 17184; 15pp; English. · 0 Kovalic DK, 84.5%; polynucleotide that can be Best Local Similarity 99.2 Matches 247; Conservative KOVALIC D K. TABASKA J E WPI; 2004-180133/17. SCREEN S E. Local Similarity Zhou Y, improving yield. 239 121 329 Query Match 61 (KOVA/) (SCRE/) (TABA/) CAOY/) Liu J,

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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance;

Plant full length insert polynucleotide segid 17184.

21-APR-2005

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28-APR-2003; 2003US-00425114.
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05-NOV-2001; 2001US-00985678.
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                                                                          67.1%;
81.5%;
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                                                                                                               Matches 243; Conservative
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(ZHOU/) ZHOU Y.
(KOVA/) KOVALIC D K.
(SCRE/) SCREEN S E.
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                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
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 invention.
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19
                                                                          Query Match
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(CAOY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA construct, useful for improving plant tolerance to cold, hear, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                   GTGGCGGGGGGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCTTTAAACTGTTGTCA 478
                                                                                                                                                                                                                                                                                                                                           plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screen SE, Tabaska JE,
                                                                                                                                                                                                                                                                                                          Plant full length insert polynucleotide seqid 15469.
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                                                                                                                                                                                          ADX32649 standard; cDNA; 807 BP
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                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein content; gene; ss.
                                                          249
                                                                                              CTTGCATT 487
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                          241
                                                                                              479
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(TABA/)
(CAOY/)
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(KOVA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACTGTTGTCGCTTGCATTTTTAACCTTTTCATCGCCGTTCAGTGGTCCTAAATCTAT 786
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                                                                                                                                                                                                                    GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTG------
                                                                                                                                                                                                                                                                                                                                          111 --TCGTCAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             609 ATTIGICGGGAAATTIGGGGGCTCCCCATATGAGATGCTGCCGGGCAAGACCTCGGCAT
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                                                                                                                                                                              1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCACCTCGTTTGTGGGGGGGGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCTTT
                                                                                                                   Gaps
                                                                                                                   12;
                                                           DB 13; Length 807;
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Sequence 807 BP; 172 A; 213 C; 214 G; 208 T; 0 U; 0 Other;
                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant full length insert polynucleotide segid 25681.
                                                                                                                      43;
                                                     Score 195.2; DB 1:
Pred. No. 6.2e-54;
0; Mismatches 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADX50941 standard; cDNA; 824 BP.
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28-APR-2003; 2003US-00425114

19-FEB-2004.

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for impressing the rate of homologous recombination in plants, for impressing the pathogen or phosphorus use and/or uptake to providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert of the content. This sequence represents a plant full length insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 AGCCGGCTTTACGTGCCTAGAAGCTAGTACCTAGTGTTTTGCTGCTGTCTAATGACACTAT 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624 ATTIGICGGGAAATTIGGGGGCTCCCCATATGAGATGCTGCCGGGCAAGACCTCGGCAT 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathogen tolerance; pest tolerance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 --TCGTCAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGCCGGCTTTATGTGCGTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCACCTCGTTTGTGGGGGGGGGGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.1%; Score 195.2; DB 13; Length 824;
81.5%; Pred. No. 6.3e-54;
ive 0; Mismatches 43; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant protectant; plant growth regulant; gene therapy; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 824 BP; 178 A; 216 C; 218 G; 212 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant full length insert polynucleotide segid 26656.
                                           Claim 1; SEQ ID NO 25681; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADX51916 standard; cDNA; 969 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein content; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 81.5
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at try. seqdata.uspto.gov/sequence.hmm?DocID:2004034888. The polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or perss, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stream of the modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert content of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        694 GCAATGTGATCTGGACCCTGGTTTCTTGGGTGCGACGCTTGTAGCAGCCGTGTTATGATT 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 --TCGTCAGTAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     754 ATTIGICGGGAAAATTTGGGGGTCCCCATATGAGATGCTGCCGGGCAAGACCTCGGCAT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286
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                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             634 AGCCGGCTTTACGTGCCTAGAAGCTAGTACCTAGTGTTTGCTGCTGTCTAATGACACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCACCTCGTTTGTGGCGGGGGGCGCTGGAGCCCGGTCTGGTTGGGAAGCCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.1%; Score 195.2; DB 13; Length 969; 81.5%; Pred. No. 6.7e-54; ive 0; Mismatches 43; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 969 BP; 218 A; 238 C; 269 G; 244 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                  Tabaska JE,
                                                                                                                                                                                                                                                                Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 26656; 15pp; English.
                                                                        06-MAY-1999; 99US-00304517.
                                                                                                                                                                                                                                                                Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 81.5
es 243; Conservative
                                                                                                                                                                                                                                                                                                       WPI; 2004-180133/17.
                                                                                                                                                                   KOVALIC D K.
                                                                                                                                                                                                         TABASKA J E
CAO Y.
                                                                                                                                                                                         SCREEN S E.
                                                                                                                                                                                                                                                                  Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                improving yield.
                                                                                                                                  LIU J.
ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                     (KOVA/)
(SCRE/)
                                                                                                                                                                                                         (TABA/)
(CAOY/)
                                                                                                                                (LIUJ/)
                                                                                                                                                     (ZHOOL)
                                                                                                                                                                                                                                                                  Liu J,
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Matches
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ADJ62814/c RESULT 11

US2004034888-A1.

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cardiovascular disease; immune system disorder; organ transplantation; tissue respeneration disorder; diabetes mellitus; hypothyroidism; choler; tissue respeneration disorder; diabetes mellitus; hypothyroidism; cholersol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antiatherosclerotic; antionflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2233; 2508pp; English.
                                                                                                                                                                                                                                                       24-MAY-2001; 2001WO-US017076.
                                                                                                                                                                                                                                                                                            24-MAY-2000; 2000US-0206690P
                                                                                                                                                                                                                                                                                                                                                               Leach MD, Shimkets RA;
                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                    2002-106200/14.
                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABP35002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplantation.
                                                                                                                                                                                  WO200190366-A2
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                     29-NOV-2001
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an array for screening a patient for resistance to docetaxel comprising complementary nucleic acid probes attached to a solid surface for at least 10 of the nucleic acids chosen from 91 fully defined sequences as given in the specification. The array is useful for screening a patient for resistance to docetaxel. The array is also useful for monitoring a cancer patient receiving docetaxel therapy. The present sequence represents a human cDNA differentially expressed in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 CTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTTGTGGCGGGGGGGCGCTGGAGCCCGGTC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Array useful for screening patient for resistance to docetaxel comprises complementary nucleic acid probes attached to solid surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 76201 BP; 19685 A; 17309 C; 18629 G; 20578 T; 0 U; 0 Other;
                                                                                                             #84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.6%; Score 33.8; DB 12; Length 76201; 64.9%; Pred. No. 12;
                                                                                                           Human cDNA differentially expressed in response to docetaxel
                                                                                                                                               docetaxel resistance; cancer; human; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; SEQ ID NO 84; 169pp; English.
   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN79028 standard; cDNA; 378 BP
   ADJ62814 standard; cDNA; 76201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 TGGTTGGGTTGGGAAGC 223
                                                                                                                                                                                                                                                                                                           16-MAY-2003; 2003US-00439703.
                                                                                                                                                                                                                                                                                                                                              17-MAY-2002; 2002US-0381141P.
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Conservative
                                                                                                                                               array, docetaxel; docete
differential expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                      O'connell P;
                                                                                                                                                                                                                                                                                                                                                                                (CHAN/) CHANG J C. (OCON/) O'CONNELL P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-224389/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                      US2004018527-A1.
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                         29-JAN-2004.
                                                                        06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang JC,
                                       ADJ62814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               docetaxel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Sequences ABP31028-ABP35561 represent 4534 novel human proteins
designated ORF (open reading frame) 1-4534, and sequences ABN75054-
ABN79697 represent cDNAs encoding them. The invention also encompasses
polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
referred to as ORFX) proteins, polymuclectides at least 85% identical to
the ORFX mucleic acid sequences, vectors and host cells comprising ORFX
polymelectides, the recombinant production of ORFX proteins, antibodies
polypeptides, methods of screening for modulators of ORFX proteins and
polypeptides, methods of screening for modulators of ORFX proteins and
collymelectides and disorder. The ORFX proteins of the invention have a wide
crange of biological activities, such as cytokine, cell proliferation,
cell differentiation, immune modulation, hammatopic of the invention have a wide
crange of biological activity, and may also be involved in the determination
cell differentiation, immune modulation, hammatopic activity,
cell differentiation, immune modulation, hammatopic activity,
cell differentiation, immune modulation, because of the invention activity,
cell differentiation, antiniffarmatory activity, thromothytic activity,
cell differentiate activity, and may also be involved in the determination
cranged and antibodies may be used in the treatment of cancers,
coll bedily characteristics, fertility and behaviour. ORRY proteins,
corpus and antibodies may be used in the treatment of cancers,
corpus transplantation, disorders of tissue growth and regeneration,
corpus transplantation, disorders of tissue growth and regeneration,
corpus transplantation, disorders of tissue growth and regeneration,
corpus transplantation, disorders of tissue growth and regeneration
corpus transplantation, disorders of tissue growth and regeneration
corpus transcriptes, in the identification and cloning of homologous
corpus adapted and probes, in the detection of ORFX genomic sequences, in generate and probes, in the detection of ORFX genomic acids may additionally be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%; Score 33.6; DB 6;
53.5%; Pred. No. 1.5;
cive 0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69; Conservative
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Matches
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Human, ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemctactic; chemokinetic; haemostatic; thrombolytic; tumour inhibin; bodily characteristic; ferrility; behaviour; cancer; proliferative disorder; neurological disorder;

Human ORF3975 cDNA, SEQ ID NO:7949.

(first entry)

08-JUL-2002

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The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to associated (CA) nucleic acids encoding them. The invention also relates to amethod for treating coancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample cartivity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a citivity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a classe. This sequence represents a human CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
  210
                                      321 dedecardeceracionerecentralecentrales de consecuencia de 262
                                                                                                                        261 GGGGGTGGGAACCTGGGAGCCCCCTTCTCCGGGGACGTGACCTGTGAGCTCCACTTTTC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer-associated protein; CAP; cancer-associated gene; CA; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human cancer associated protein encoded within open reading frame
  CGGGCAAGGCCTCGGTGTCCCACCTCGTTTGTGGCGGGGGGGCGCTGGAGCCCGGTCTGGT
                                                                               211 TGGGTTGGGAAGCCCTTTAAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56826 BP; 13146 A; 14623 C; 15023 G; 14034 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer associated gene, useful as targets for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 56826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer-associated (CA) gene HD07-096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.2; 1
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; SEQ ID NO 664; 182pp; English.
                                                                                                                                                                                                                                                                                                                ABD33496 standard; DNA; 56826
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Best Local Similarity. 59.6%;
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; cancer; cytostatic.
                                                                                                                                                               271 TTGTGAGTG 279
                                                                                                                                                                                                        201 CCGAGGGG 193
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151
                                                                                                                                                                                                                                                                                                                                                         ABD33496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequence (ABL16176-ABL30511), expressed DNA ABR2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTATGCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 33796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 33796; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from WIPO at ftp.wipo.int/pub/published_pct_sequences
                           10198 GGGGTCGGGCTCTGGGTCTGCGTAGGCTGGG 10165
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214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32.8; DB pred. No. 7.2; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
                                                                                                       ABL27441 standard; DNA; 3879
                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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53.0%;
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                                                                                                                                                                    (first entry)
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genes from Drosophila and
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                                                                                                                                                                                                                                                 pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
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                                                                                                                                                                    26-MAR-2002
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10258 AATGGAGGCCTCCCCCCTCTCCCCACCATCCCGCGTCGTCACCCCCCTGCTT 10199

121 AATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCACCTCGTTT 180

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3019 CACTGCTCAGTGTGGAGTCTAGAATTATTTCCACGGTGCCATCGTCCTTGTGACTGGAGT 2960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                           Drosophila melanogaster genomic polynucleotide SEQ ID NO 33793.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 33793; 21pp + Sequence Listing; English.
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                                           ABL27440 standard; DNA; 6613 BP.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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                                                                                                                                                                                            26-MAR-2002
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                                                                                                                      ABL27440;
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Search completed: March 8, 2006, 04:18:55 Job time : 340.308 secs

AC125979 Rattus no AC109699. Rattus no AC10969. Rattus no AC150176 Gallus ga AC07111 Homo sapi AC05125 Pan trogl AC09056 Homo sapi AC010994 Drosophil AC010994 Drosophil AC010994 Drosophil AC01083 Homo sapi AC010843 Drosophil AC01674812 Sequence V48224 Human beade AC055753 Homo sapi

ACO76965 Homo eapl ALS90503 Mouse DNA ACL53845 Mus muscu ACL59467 Mus muscu ACL59467 Mus muscu ACL59467 Mus muscu ACL59473 Rattus no ACL28473 Rattus no

PLN 27-OCT-2004

252

9

Gaps

8

score:

Title:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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2 (bases 1 to 1189)
Lai,J., Dey,N., Kim,C.-S., Bharti,A.K., Rudd,S., Mayer,K.F.X.,
Larkins,B., Becraft,P. and Messing,J.
Submission
Submitted (27-OCT-2004) Waksman Institute, Rutgers University, 190
Frelinghuysen Rd, Piscataway, NJ 08854, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Lai,J., Dey,N., Kim,C.-S., Bharti,A.K., Rudd,S., Mayer,K.F.X.,
Larkins,B., Becraft,P. and Messing,J.
Characterization of the maize endosperm transcriptome and its
comparison to the rice genome
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Zea mays clone EL01N0450F06.c mRNA sequence.
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Pred. No. 9.5e-61;
0; Mismatches 8
                                 AC007111
AC0154112
AC0154112
AC009065
AC012171
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/mol_type="mRNA"
/db_xref="taxon:4577"
/clone="EL01N0450F06.c"
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AC161746
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Matches 283; Conservative,
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DEFINITION
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AUTHORS
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                                                                         8, 2006, 03:57:42 ; Search time 2087.91 Seconds (without alignments) 7922.477 Million cell updates/sec
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                                                                                                                                             agccggctttatgtgcgtag.........tgtgagtggtcctatatcaa 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                   5883141 segs, 28421725653 residues
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                     nucleic search, using sw model
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BT016497
MZEREGP
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BV150856
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Maximum DB seq length: 200000000
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291
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Best Local Similarity 99.2%;
Matches 261; Conservative
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Greedaaaarrregegegerecegraaggargereceregeaaggeeregereregrangs 132
                                                                                                      CCTCGTTTGTGGGGGGGGGGGCGCTGGAGCCCGGTCTGGGTTGGGTTGGGAAGCCCTTTAAAC 232
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1 (bases 1 to 320)
Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
Ty UTR sequences of maize genes
Unpublished (2001)
                                                                                                                                    ccrcercreresceresceceresascecestrescriescriescaascecerraaae 72
                                                                                                                                                                 233 TGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA 291
                                                                                                                                                                                genomic
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60 degrees C for 45 seconds
72 degrees C for 90 seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Schnable, P.S.
Schnable laboratory
Iowa State University
G405 Agronomy Hall, Ames, IA 50011, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Primer A: GAGCGAGGAGTCCTACAAGG
Primer B: GCGATGGAAAAGGTPAAAATGC
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4577"
/clone lib="maize leaf DNA"
/note="PCR products amplified
<1. .>320
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Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total vol: 20 ul
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Polymerization: 72 degrees C
PCR cycles: 31
Thermal cycler: Perkin Elmer
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/mol_type="genomic DNA"
/strain="DE811"
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Tris-HCl: 20 mM
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G71239.1 GI:14332924
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AUTHORS
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DB 10; Length 320;

89.3%; Score 259.8;

Query Match

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CDGILKLLETHILVPSSTABEKKPYLYKMKGDYYRYLAREKTGARERKDAAENTWAYKA
AQDIALAELAPTHPIRGIALINFSVEYYETINSPDRACSLAKQAFDEAISELDTLSEE
SYKDSTLIMQLIKDNITLWTSDISEDPAEEIRRAPKRDSSEGQ"
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                                                                                                                                             58 AGCCGGCTTTATGTGCCTAGAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT 117
                                                                                                                                                                                                                                                                118 GCAATGTGATCTGGAACCTGGTTTCTTGGATGCGACGCTTGTTATGACTGTCGTCAGTAA 177
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1 (bases 1 to 5348)

de Vetten, N. C. and Ferl, R. J.

de Vetten, M. C. and Ferl, R. J.

expression, and potential regulation by the G-box binding complex Plant Physiol. 106 (4), 1593-1604 (1994)
                                                                                         9
                                                                                                                                                                                                           61 GCAATGTGAATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA
                                                                                                                                                                                                                                                                                                                                                                                     178 AATTIGGGGCTCCCCGTATGAGAIGCTGCCGGCAAGGCCTCGGTGTCCCACCTCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GTGGCGGGGGGCGCTGGAGCCCGGTCTGGTTGGGAAGCCCTTTAAACTGTTGTCA
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join(2177. .2583,2671. .2749,2876. .2998,4387. .4503,
4610. .4669)
/gene="GRF1"
                           Gaps
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/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
join(1491. .2583,2671. .2749,2876. .2998,4387. .4503,
4510. .4669
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entry [NCBI gibbsq 164519] from the original journal article.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.9%; Score 258.6; DB 15; Length 5348; Best Local Similarity 94.3%; Pred. No. 2.6e-60; Matches 282; Conservative 0; Mismatches 9; Indels 8;
                              ö
                              Indels
Pred. No. 1.2e-60;
); Mismatches 2;
                                                                                      1 AGCCGGCTTTATGTGCGTAGAAACTAGTAGCTAGTGTT
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/codon_start=1
/product="GF14-6"
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/db_xref="GI:998430"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGCATTTTACCTTTTCCATCG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 CTTGCATTTTACCTTTTCCATCG 263
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PLN 27-0CT-2004
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2 (bases 1 to 1194)
Lai,J., Dey,N., Kim,C.-S., Bharti,A.K., Rudd,S., Mayer,K.F.X.,
Larkins,B., Becraft,P. and Messing,J.
Direct Submission
Submitted (27-OCT-2004) Waksman Institute, Rutgers University, 190
Frelinghuysen Rd, Piscataway, NJ 08854, USA
Location/Qualifiers
                                                                                                                                                                                                                       114 AGCCGGCTTTATGTGCCTAGAAACTAGTAGCTAGTGTTTGCTGCTGTCGAATGACACTAT 173
                                                                                                                                                                                                                                                                 61 GCAATGTGAICTGGAACCTGGTTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112
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1 (bases 1 to 1194)

Lai,J., Dey,N., Kim,C.-S., Bharti,A.K., Rudd,S., Mayer,K.F.X., Lai,J., Dey,N., Kim,C.-S., end Messing,J.

Characterization of the maize endosperm transcriptome and its comparison to the rice genome
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Best Local Similarity 81.5%; Pred. No. 7.4e-43;
Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps
                                                                                                                                          Gaps
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8
/note="PCR products amplified from genomic DNA'
<1. .>372
                                                                                          Length 372;
                                                                                          Score 220.2; DB 10; Length
Pred. No. 9.8e-50;
0; Mismatches 8; Indels
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BT016497
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/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone="Contig330"
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FLI_CDNA.
Zea_mays
Zea_mays
                                                                                            75.7%;
93.8%;
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Best Local Similarity 93.84
Matches 243; Conservative
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        4790 GTCCGTAAAATTTGGGGGCTCCCCGTAAGGGATGCTGCCTGGCAAGGCCTCGGTGTCCCA 4849
                                                                                                                                                                                                                                                                                           4850 CCTCGTCTGTGGCGTGGGGCGCTGGAGCCCGGTCTGGTTGGGAAGCCCTTTAAAC 4909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G70551
716223731FB73 maize leaf DNA Zea mays STS genomic, sequence tagged
                                                                                                                                                                             113 GTCAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCCA 172
                                                                                                                                                                                                                                                              173 CCTCGTTTGTGGGGGGGGGGCGCTGGACCCGGTCTGGTTGGGTTGGGAAGCCCTTTAAAC 232
                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Spermatophyta, Spermatophyta, Spermatophyta, Bagnoliophyta, Bagnoliophyta, Ballophyta, Banicoldeae, Andropogoneae; Zea.

1 (bases 1 to 372)

1 (bases 1 to 372)

3 (Baray, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.

3 UTR sequences of maize genes
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                  233 TGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA 291
                                                                                          61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCT-----AGTTATGACTGTC
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seconds
seconds
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Schnable laboratory
Iowa State University
G405 Agronomy Hall, Ames, IA 50011, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Primer A: GAGGGAGGAGTCCTACAAGG
Primer B: GCGATGGAAAAGGTAAAATGC
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 degrees C for 30
60 degrees C for 45
72 degrees C for 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Template: 10-20 ng
Primer: each 0.5 uM
dNTPB: each 200 uM
Tag Polymerase: 0.05 units/ul
Total vol: 20 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR cycles: 31
Thermal cycler: Perkin Elmer TC
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/clone_lib="maize leaf DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="DE811"
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Location/Qualifiers
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Tris-HCl: 20 mM
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G70551.1 GI:14332236
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Polymerization:
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Zea mays
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

ACCESSION

916

source

FEATURES

us-10-603-524a-2.rge

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941 CCCCCACCTCGTTTCAGGCGGGGACGCTGGAGCCTGGTCCGGTTGGGTTCGGAAGCCCC 1000
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                               1 (Dases 1 to 327)
McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S.,
Sanchez-Villeda,H., Houchins,K., Fang,Z., Polacco,M., Gardiner,J.
and Coe,E.H.Jr.
MMP SNP Discovery
Unpublished (2003)
                                                                                                GTCCCACCTCGTTTGTGGCGGGGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCT
                                                                              TTAAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT
                                                                                                                                                                                                            BV150852 327 bp DNA linear STS 11-MAY·
PZA02088-74466-B73 Zea mays B73 Zea mays STS genomic, sequence
tagged site.
BV150852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABI protocol - using d-Rhodamine terminator cycle sequencing ready reaction with amplifaq DNA polymerase FS Sequence ran on ABI 3700 sequencer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize Mapping Project
University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 5738827606
Fax: 5738847850
Famall: WohullenWemissouri.edu
Primer A: CTATGCAATGTGATCTGGACCTG
Primer B: TAAGATGGGATGGGACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protocol:
PCR amplification of genomic DNA
Solution of genomic DNA
Solution of genomic DNA
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Total Vol:
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each 200 uM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Michael D. McMullen
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Location/Qualifiers
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Redraq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
                                                                                                                                                                                                                                                                                         GI:47100309
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Primer:
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   167
                                                                            227
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BV150852
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Vigarrasmiissieokeegkgnedrulikdyrgieteteltkicogilklleshlv
Sestapeskyvylkwkgdyryviaefkytgaerkoaaenymvaykaaqdialaelapth
Pirlolalmysvpyystilnspdracsilakoapbracsilkoerdiseldytlseesykdstlimollh
Dnltilwysdisedppaeeireapkholsegq
                                                                                                1037 CCCACCTCGTTTCAGGCGGGGACGTGGTGCGTGGTCGGGTTGGGGAAGCCCCTT 1096
                                   977 ATCCCTCGGGAAATTTGGGGGCTCCCCATATGAGATGCTGCCGGGAAGACCTCGGCAT 1036
                                                                                                                                                                                                                                                                                       27-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD Clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 1082)
de Vetten,N.C., Lu,G. and Peri,R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761 AGCCGGCTTTACATGCCTAGAAGCTAGTACCTAGTGTTTTGCTGCTGTCTAATGACATTAT 820
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                                                                                                                                                                     1097 AAACTGTTGTCGCTTTGTAACCTTTTCATCGCCGTTCAGTGGTCCTAAATCTAT 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original source text: Zea mays (strain P3377) (library: R.J.Ferl) 
CDNA to mRNA.
                                                                                                                                                   229 AAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTC----
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                                                                          169 CCCACCTCGTTTGTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCCGGCTTTATGTGCGTAGAAACTAGTAGTAGTGTTTTGCTGCTGTCGAATGACACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ue vetten,N.C., Lu,G. and Feri,R.J.
A maize protein associated with the G-box binding complex has homology to brain regulatory proteins
Plant Cell 4 (10), 1295-1307 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.0%; Score 183.2; DB 15; Length 1082; Best Local Similarity 81.0%; Pred. No. 1.5e-39; Matches 243; Conservative 0; Mismatches 43; Indels 14; Gaps
                                                                                                                                                                                                                                                                       MZEREGP 1082 bp mRNA linear PLN
Zea mays regulatory protein GF14-12 mRNA, complete cds.
M96856
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/organism="Zea mays"
/mol type="mRNA"
/strain="P37"
/db xxef="taxon:4577"
/map="25"
/cell type="suspension cell"
/tissue lib="R.J.Perl"
1. .1082
/gene="GF14-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="regulatory protein"
/protein_id="AAA33505.1"
/db_xref="GI:168603"
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MZEREGP
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Zea mays
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PZAO2088-74468-CO159 Zea mays STS genomic, sequence
tagged site.
                                                                                                                                                                                                                                                                          112
                                                                                                                                                                                                                                                                                                                                                                       61 ATTIGTCGGGAAAATTTGGGGGCTCCCCATATGAGATGCTGCCGGCAAGACCTCGGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panticoideae; Andropogoneae; Zea.

(Dases 1 to 338)

McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S., Sanchez-Villeda,H., Houchins,K., Fang,Z., Polacco,M., Gardiner,J. mMP SNP Discovery

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                  113 ----GTCAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGT 168
                                                                                                                                                                                                                                                                                                                                                                                                                         169 CCCACCTCGTTTGTGGCGGGGGGCCTGGAGCCCGGTCTGGTTGGGAAGCCCTTT 228
                                                                                                                                                                                                                                                                                             1 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTGAGCAGCCGTGTTATGATT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                                                                                                                                                                                                                                                                          61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTC-----
                                                                                                                                                                                                                                       Gaps
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                              /mol_type="genomic DNA"
/cultivar="B73"
/db.txef="texnon:4577"
/clone_lib="Zea mays B73"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. >327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABI protocol - using d-Rhodamine terminator cycle sequencing ready reaction with amplifag DNA polymerase Sequence ran on ABI 3700 sequencer.
                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                 DB 10; Length 327
                                                                                                                                                                                                                                     0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize Mapping Project
University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
Tel: 5738827606
Fax: 5738847850
Email: McMullenN@missouri.edu
Email: A: CTARGCAAGTGTGATCTGAACCTG
Primer A: CTARGCAAGTGTGATCT
                                                                                                                                                                                             Score 144.8; DB 1
Pred. No. 5.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR amplification of genomic DNA Template: 50 ng
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1. .327
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Michael D. McMullen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BV150853.1 GI:47100310
                                                                                                                                                                                               tch 49.8%; al Similarity 79.4%; 189; Conservative (
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Zea mays
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Matches 18
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JOURNAL
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KEYWORDS
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                                                                113 ----GTCAGTAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATTIGICGGGAAAATTIGGGGGGTCCCCATAIGAGAIGCTGCCGGGCAAGACCTCGGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCACCTCGTTTGTGGCGGGGGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCTTT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 318)

McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S., and Coe,E.H.Jr.

McMob SNP Discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                           AAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                                                                  338 bp DNA linear STS 11-MAY.
PZA02008-74483-ILO Zea mays ILO Zea mays STS genomic, sequence
tagged site.
BVI50856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTAGCAGCCGTGTTATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4577"
/dlone_lib="Zea mays CO159"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .>338
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 49.8%; Score 144.8; DB 1. 79.4%; Pred. No. 5.6e-29; ive 0; Mismatches 37
                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/cultivar="CO159"
                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
Genomic DNA amplification
Redrag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BV150856.1 GI:47100313
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BV150858 338 bp DNA linear STS 11-MAY-2004
PZA02088-74469-Mp708 Zea mays Mp708 Zea mays STS genomic, sequence
                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                 1 (bases 1 to 338)
McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S.,
Sanchez-Villeda,H., Houchins,K., Fang,Z., Folacco,M., Gardiner,J.
and Coe,E.H.Jr.
MMP SNP Discovery
Unpublished (2003)
   229 AAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                   181 AAACTGTTGTCGCTTGCATTTTAACCTTTTCATCGCCGTTCAGTGGTCGTCAAAATCTAT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABI protocol - using d-Rhodamine terminator cycle sequencing ready reaction with amplifaq DNA polymerase FS Sequence ran on ABI 3700 sequencer.
                                                                                                                                                                                                                                                                                                                                                                                                                   Maize Mapping Project
University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 5738827606
Fax: 5738847850
Famil: WohullenWemissouri.edu
Primer A: CTATCCAATGTGATCTGGAACTG
Primer B: TAAGATGGGATGGGGACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR amplification of genomic DNA Template: 50 ng Primer: each 0.5 uM dNTPs: each 200 uM Taq Polymerase: RedTaq (Sigma) Total Vol: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DNA"
/cultivar="Mp708"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .338
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Michael D. McMullen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic DNA amplification
Redraq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
                                                                                                                                                                            GI:47100315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amplicon sequencing
                                                                                                                                             tagged site.
                                                                                                                                                             BV150858
BV150858.1
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                                                                                                                                                                                                             Zea mays
                                                                                                                                                                                                                          Zea mays
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                                                                                                              LOCUS
DEFINITION
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATTTGTCGGGAAAATTTGGGGGCTCCCCATATGAGATGCTGCCGGCAAGACCTCGGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCACCTCGTTTCAGGCGGGGGGCGCTGGAGCGTGGTCCGGTTGTTGGGAAGCCCCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTAGCAGCCGTGTTATGATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 ----GTCAGTAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCACCTCGTTTGTGGGGGGGGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGGAGCCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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sequencing ready reaction with amplifag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_rref="taxon:4577"
/clone_lib="Zea mays ILO"
/dev stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
49.8%; Score 144.8; DB 10; Length 338;
Best Local Similarity 79.4%; Pred. No. 5.6e-29;
Matches 189; Conservative 0; Mismatches 37; Indels 12;
                                               Maize Mapping Project
University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
                                                                                            Tel: 5738827606
Fax: 5738847850
Faxil: McMullenMemissouri.edu
Primer A: CTATCCAATCTGGATCTGGAACTG
Primer B: TAAGATGGGATGGGACAAT
                                                                                                                                                                         Protocol:
PCR amplification of genomic DNA
Template:
50 ng
Primer:
each 0.5 uM
dNTP8:
each 200 uM
Taq Polymerase: RedTaq (Sigma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="ILO"
                                Contact: Michael D. McMullen
                                                                                                                                                                                                                                                                                                                                                                   Buffer:
Genomic DNA amplification
                                                                                                                                                                                                                                                                                                                                                                                                 RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
                                                                                                                                                                                                                                                                          10 ul
                                                                                                                                                                                                                                                                                       Amplicon sequencing
Unpublished (2003)
                                                                                                                                                                                                                                                                          Total
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d-Rhodamine kit (ABI)
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KEYWORDS
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STS
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BV150861
LOCUS
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PZA02088-74481-NC7A Zea may8 NC7A Zea mays STS genomic, sequence
                                                                                                                                                                                                                                                                                       61 ATTIGTCGGGAAAATTIGGGGGCTCCCCATATGAGAIGCTGCCGGGCAAGACCTCGGCAT 120
                                                                                                                                                                                                                                                                                                                                                           61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTC----- 112
                                                                                                                                                                                                                                                                                                                                      169 CCCACCTCGTTTGTGGGGGGGGGCGCTGGGCCCGGTCTGGTTGGGAAGCCCTTT 228
                                                                                                                                                                                                                   1 GCAATGTGAATCTGGAACCTGGTTTTTTTGGGGGGCGACGCTTGTAGCAGCCGGGTTATGATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S.,
Sanchez-Villeda,H., Houchins,K., Fang,Z., Polacco,M., Gardiner,J.
                                                                                                                                                                                                                                                                                                                                                                                                            229 AAACTGTTGTCACTTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                113 ----GTCAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGT
                                                                                                                                                             Gaps
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/dev_stagc="seedlings"
/not="Organ: leaf; genomic DNA from inbred line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplifag DNA polymerase
Sequence ran on ABI 3700 sequencer.
                                                                                                                                                            12;
                                                                                                                       Score 144.8; DB 10; Length 338;
Pred. No. 5.6e-29;
0; Mismatches 37; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize Mapping Project
University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 5738827606

Fax: 5738847850

Famil: McMullenW@missouri.edu

Primer A: CTATGCAATGTGATCTGGAACCTG

Primer B: TAAGATGGGGATGGGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dNTPs:
cach 0.5 uM
dNTPs:
cach 0.5 uM
Tag Polymerase: RedTag (Sigma)
Total Vol:
nmplicon sequencing
ABI profi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR amplification of genomic DNA
Template: 50 ng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Michael D. McMullen
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RedTaq (Sigma)
Sequencing buffer
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                                                                                                                       49.8%;
ilarity 79.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Coe, E.H.Jr.
MMP SNP Discovery
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tagged site.
                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
Zea mays
                                                                                                                                                          189;
                                                                                                                       Query Match
Best Local S:
Matches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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JOURNAL
COMMENT
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BV150859
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STS 11-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCACCTCGTTTGTGGCGGGGGGGCCTGGACCCGGTCTGGTTGGGAAGCCCTTT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CCCACCTCGTTTCAGGCGGGGGCGCTGGAGCGTGGTCCGGTTGTGTTGGAAGCCCCTT 180
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PZA02088-74480-Tx303 Zea mays Tx303 Zea mays STS genomic, sequence
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S.,
Sanchez-Villeda,H., Houchins,K., Fang,Z., Polacco,M., Gardiner,J.
and Coo.E.H.Jr.
MMP SNP Discovery
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GTCAGTAAAATTTGGGGGGCTCCCCGTATGAGATGCTGCCGGGCCAAGGCCTCGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTTATGACTGTC-----
Gaps
                                       889
990
990
890
73
        58
                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4577"
/clone_lib="Zea mays NC7A"
/dev_stage="seedling"
/note="organ: leaf; genomic DNA from inbred line"
<1. .>338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 144.8; DB 10; Length
Pred. No. 5.6e-29;
); Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/cultivar="NC7A"
                                                                                                                                                                                                                                                                                                     1. .338
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Michael D. McMullen
Maize Mapping Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.4%; Pre
Matches 189; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BVI50861
BV150861.1 GI:47100318
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BV150863 338 bp DNA linear STS 11-MAY-2004 PZA02088-74482-W22_R-scm2 Zea mays W22_R-scm2 Zea mays STS genomic,
                                                                                                                                                                                                                                                                                                              Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 338)

McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S.,
and Coe,E.H.Jr.

AMP SNP Discovery

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABI protocol - using d-Rhodamine terminator cycle sequencing ready reaction with amplifaq DNA polymerase FS Sequence ran on ABI 3700 sequencer.
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/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize Mapping Project
University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
701 S13827606
Fax: 5738847850
Email: McMallandemissouri.edu
Friner A: CTATGCAATGTCAACTGGAACCTG
Primer B: TAAGATGGGATGGGACAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protocol:
PCR amplification of genomic DNA
Template: 50 nd
Primer: each 0.5 uM
dNTPs: raq Polymerase: Redrag (Sigma)
Total Vol: 10 ul
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/cultivar="W22_R-scm2"
/db_xref="taxon:4577"
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1. .338
/organism="Zea mays"
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Genomic DNA amplification
Redraq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
                                                                                                                                                                                                                    BV150863.1 GI:47100320
                                                                                                                                                       sequence tagged site.
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                                                                                                                                                                                                                                                                                           Zea mays
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                                RESULT 13
BV150863
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AUTHORS
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sequencing ready reaction with amplifag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
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University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
711: 5738827606
Fax: 5738847850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/culfivar="Tx303"
/db_xref="taxon:4577"
/clone lib="Zea mays Tx303"
/dev_stage="seedling"
                                                                                                                Email: McMullenM@missouri.edu
Primer A: CTATGCAATGTGATCTGGAACCTG
Primer B: TAAGATGGGATGGGACAGAAT
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PCR amplification of genomic DNA
Template:
Formar:
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/organism="2ea mays"
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Sequencing buffer
d-Rhodamine kit (ABI)
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T218 Zea mays STS genomic, sequence
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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230 AACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
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/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .>325
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Maize Mapping Project
University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
721: 5738827606
Fax: 5738847850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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Pred. No. 1e-28;
0; Mismatches
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/cultivar="Tx501"
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/organism="Zea mays"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S.,
Sanchez-Villeda,H., Houchins,K., Fang,Z., Polacco,M., Gardiner,J.
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sequencing ready reaction with amplifag DNA polymerase
Sequence ran on ABI 3700 sequencer.
                                                                                                                                    12;
                                                                                  DB 10; Length 338;
                                                                                                                                    Indels
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University of Missouri-Columbia
301 Curtis Hall, Columbia, Mo 65211-7020, USA
738827606
Fax: 5738847850
Email: McMullenN@missouri.edu
Primer A: CTATGCAATGTGATCTGAACCTG
Primer B: TAAGGATGTGATCAAAT
                                                                                                                              37;
                                                                               Score 144.8; DB 1
Pred. No. 5.6e-29;
0; Mismatches 37
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tagged site.
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Best Local Similarity 79.4%;
Matches 189; Conservative
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MMP SNP Discovery
Unpublished (2003)
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 ---GTCAGTAAAATTTGGGGGCTCCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 CCACCTCGTTTGTGGCGGGGGGCGCTGGGTCTGGTTGGGTTGGGAAGCCCTTTA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTAGCAGCCGTGTTATGATTA 60
                                                                                                                                                                                                                             230 AACTGTTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AACTGTTGTCGCTTTTTAACCTTTTCATCGCCGTTCAGTGGTCCTAAATCTAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 49.4%; Score 143.8; DB 10; Length 327; Best Local Similarity 79.3%; Pred. No. 1e-28; Matches 188; Conservative 0; Mismatches 37; Indels 12; Gaps
                                                                                                                                                                                                               Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplifag DNA polymerase FS
sequence ran on ABI 3700 sequencer.
                                                                                                                                                                                                                                                                                                                                                                                        Email: McMullenM@missouri.edu
Primer A: CTATGCAATGTGATCTGGAACCTG
Primer B: TAAGATGGGATGGGACAAAT
                              Protocol:
PCR amplification of genomic DNA
Template: 50 ng
                                                          dNTPs: each 0.5 uM dNTPs: each 200 uM Taq Polymerase: RedTaq (Sigma) Total VO: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                       Buffer:
Genomic DNA amplification
                                                                                                                                                                           RedTag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STS
ORIGIN
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Search completed: March 8, 2006, 06:32:12 Job time : 2091.91 secs